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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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## TITTY NOT TIT	OM nucleic - nucleic search, using sw model	
### 199-10-043-539A-1  ###################################	on: November 17, 2003, 09:13:37; Seard: (without 10496.18	time 3691 Seconds lignments) Million cell updates/s
rable: IDENTITY_NUC  Gapop 10.0, Gapaxt 1.0  2888711 seqs, 20454813386 residues  mber of hits satisfying chosen parameters:  5777422  Baseq length: 200000000  cessing: Minimum March 0%  Maximum March 10%  Miximum March 10%  Lis db ba:*  2: gb ha:*  2: gb ha:*  3: gb ha:*  4: gb on:*  6: gp on:*  7: gp on:*  11: gb on:*  8: gp on:*  11: gb on:*  12: gb on:*  13: gb on:*  14: gb on:*  15: gb on:*  16: em fun:*  17: em fun:*  18: em fun:*  18: em fun:*  18: em fun:*  22: em fun:*  23: em fun:*  24: em fun:*  25: em fun:*  26: em fun:*  27: em fun:*  28: em fun:*  28: em fun:*  29: em fun:*  20: em fun:*  20: em fun:*  20: em fun:*  21: em fun:*  22: em fun:*  23: em fun:*  24: em fun:*  25: em fun:*  26: em fun:*  27: em fun:*  28: em fun:*  29: em fun:*  20: em fu	US-10-043-539A-1 score: 947 :: 1 gttttcaaaatcggtggagg	9.4
mber of hits satisfying chosen parameters: 5777422  BB seq length: 200000000  B seq length: 200000000  Gessing: Minimum Match 100* Maximum Match 100* Maximum Match 100*  Is gb_ba: *	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.	
mber of hits satisfying chosen parameters:  DB seq length: 2000000000  DB seq length: 2000000000  Cessing: Minimum Match 100%  Listing first 45 summaries  Genembl:*  1: gb ba:*  3: gb_ln:*  4: gb_on:*  5: gb_ln:*  6: gb_ln:*  7: gb_ph:*  8: gb_ln:*  10: gb_ph:*  11: gb_sts:*  11: gb_sts:*  11: gb_sts:*  12: gb_ln:*  13: gb_ln:*  14: gb_ln:*  15: gb_ln:*  16: em_fun:*  17: em_ln:*  18: em_ln:*  18: em_ln:*  19: em_nn:*  20: em_on:*  21: em_or:*  22: em_lo:*  23: em_ltg_ln:*  24: em_ltg_ln:*  25: em_ltg_ln:*  26: em_rc:*  27: em_ltg_ln:*  28: em_ltg_ln:*  29: em_ltg_ln:*  30: em_ltg_ln:*  31: em_ltg_ln:*  32: em_ltg_ln:*  33: em_ltg_ln:*  34: em_ltg_ln:*  35: em_ltg_ln:*  36: em_ltg_ln:*  37: em_ltg_ln:*  38: em_ltg_ln:*  38: em_ltg_ln:*  39: em_ltg_ln:*  30: em_	earched: 2888711 segs, 20454813386 residue	
DB seq length: 0  DB seq length: 200000000  Listing first 45  Listing first 45  Listing first 45  ConEmbl:*  1: gb_ba:*  3: gb_ln:*  4: gb_on:*  5: gb_ph:*  6: gb_pr:*  11: gb_bs:*  11: gb_bs:*  12: gb_pr:*  13: gb_ln:*  14: gb_on:*  15: gb_pr:*  11: gb_st:*  11: gb_st:*  12: gb_st:*  11: gb_st:*  12: gb_rn:*  13: gb_pr:*  14: gb_on:*  15: gb_pr:*  16: em_bn:*  17: em_ba:*  18: em_ln:*  18: em_ln:*  18: em_ln:*  19: em_on:*  20: em_on:*  21: em_or:*  22: em_on:*  23: em_lcg_ln:*  24: em_ph:*  25: em_lcg_ln:*  26: em_lcg_ln:*  27: em_ste:*  28: em_lcg_ln:*  39: em_lcg_ln:*  38: em_lcg_ln:*  48:	number of hits satisfying chosen parameters:	5777422
Maximum Match 0%	DB seq length: 0 DB seq length: 20000000	
e:	Minimum Match 0% Maximum Match 100 Listing first 45	
11.	e:	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	% Sult Query No. Score Match Length DB ID	1 947 100.0 947 1 AF207701 Staphyl	2 826.4 87.3 304050 1 AP004829 AP004829 SCAPINIO	3 826.4 87.3 307.75 I APOUSISS ACCEPTAGE AFOODS OF STREET	4 824.8 87.1 348650 I APCUSS64 AECUSS64	5 369'8 ASSOciated Association and additional additiona	6 307 32.4 300698 1 AECUE/50 AECUE/30 AECUE/30 SCREPTIFICA	7 199.4 21.1 834 6 AXSZU416 AXSZU416 AXSZU416 SEQUENC	8 96.2 10.2 8056 6 AX599046 AX599046 AX599040 BELIEF	9 92.8 9.8 170627 2 AC125567 AC125567 AC12556 PATENS	10 91.4 9.7 67970 3 PFMALIP3 ALUST/46	TOURS THE PROPERTY OF THE PROP	12 90.4 9.5 88826 3 FFMALSES ALCOSTOR FIRSTINGS	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	87.2 9.2 80.5 6 AX598900 AX598900 AX598900 Sequence	16 85.2 9.0 286208 2 AC117140 AC117140 Rate	17 85 9.0 840 8 CNS018QK AL110675 Botx	18 84.8 9.0 2009 6 AX457067 AX457067 Sequ	19 84.6 8.9 250029 3 AE014820 AE014820 Plas	0 84.2 8.9 259474 9 HUAC004605 AC004605 HOMC	1 83.6 8.8 175544 2 AC117342 AC117342 Ratt	22 83 8.8 137411 9 AC092066 AC092066 HOMG	82.8 8.7 1090 3 ABU84/61 ABU84/61 ABU84/61	02.0 0.100.0 0.100.0 0.000.0 0	25 62.1 A. 1349980 6 AX344555 AX344555 Sequence of the control of	27 82.2 8.7 196875 2 AC098095 AC098095 Ract	28 82 8.7 6292 6 AX251493 AX251493 Sequ	29 82 8.7 233877 9 AC093798 AC093798 Homo sa	0 81.6 8.6 349751 3 PFMAL4P3 AL035476	1 81.4 8.6 156060 2 AC004153 AC004153 P.Tagnod	2 81.4 8.6 250707 3 AE014848 AE014848 P.T.S.	33 81.4 8.6 347050 3 PFA929351 AL929351	54 BL.C 0.0 99000 L ALLOONO DEWAYLLO OO TOWN THEFT OF THE CONTRIBUTION OF THE CONTRIBU	35 01.2 0.0 11.00.00 2 FIFTHALTS 0.00.01.00.00.00.00.00.00.00.00.00.00.00	20 CIT 0 C 1670404 C TITERIA DE 1670405 C TITERIA D	7 01 0 10 10 10 10 10 10 10 10 10 10 10 1	SO OF STATES STATES OF STA	AN BO B R RAFAS R PROGRESS BODI	1 80 6 8 5 313050 3 PFA929352 AL929352 Plasmod	42 RO R R R R R R R R R R R R R R R R R R	43 80 2 8 5 60604 2 AC023466 ACM AC023466	44 80 2 8 5 181792 9 AC098822 Homo sap	5 8 4 112695 8 AC119418 Medicago
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## ALIGNMENTS

AF207701 Stabhylococcus aureus putative transposase gene, partial cds; and AF207701 AF207701 AF207701.1 GI:11493941 Staphylococcus aureus Bacteria; Firmicutes; Bacillales; Staphylococcus. 1 (bases 1 to 947) Charagree, L. and Manna, A.C. Charagree, A.L. and Manna, A.C. Charagree, A.C. and Charagree, Charagree, A.C.	What linear BCT 01-DEC-2000 posase gene, partial cds; and aphylococcus.
Characterization of Sarity a modulation of	
Characterization of sarR, a modulator of	r of sar expression in
Cheung, A.L. and Manna, A.C.	-
1 (bases 1 to 947)	
Bacteria; Firmicutes; Bacillales; Staphyl	aphylococcus.
Staphylococcus aureus	
Staphylococcus aureus	
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AF207701.1 GI:11493941	
AF207701	
Sark (sark) gene, complete cds.	
Staphylococcus aureus putative transposas	posase gene, partial cds; and
AF207701 947 bp DNA	WA linear BCT 01-DEC-2000

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721 CAAGGTACACTACTTTTTTTTTTTTTTTTTTTTAAAATCAAGTTTACGATCATAA 780
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Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
Kikuchi,H.
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Submitted (06-MAR-2002) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center; Zchome 49-10 Nishinara, Shibuya-ku, Tokyo 151-0066, Japan
(E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
                                          GTTTATGTTACAGATACACAAAAAGCAAATATTCAAAAACTGATTTCAGAATTAGAAGAA
                                                                             541 TACATTAAAATTAAATCAAGGTTAATTGCGTTTAATAACATTGAACGATAACAATTTAT
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                         Staphylococus aureus subsp. aureus MW2 DNA, complete genome, strain:WM2, section 8/10.
AP004829 BA000033
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Unpublished

2 (bases 1 to 947)

Cheung, A.L. and Manna, A.C.
Cheung, A.L. and Manna, A.C.
Direct Submission
Submitted (22-NOV-1999) Microbiology, Dartmouth Medical School,
College St., Varil 206, Hanover, NH 03755, USA
Location/Qualifiers
Location/Qualifiers
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100.0%; Score 947; DB 1; Length 947;
Best Local Similarity 100.0%; Pred. No. 7.7e-126;
Matches 947; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                       note="regulatory gene'
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Whole genome sequencing of meticillin-resistant Staphylococus
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Submitted (30-JAN-2001) Director-General, Biotechnology Center, Autional Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:blo@nite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13701842.
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Staphylococcus aureus subsp. aureus N315
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/transl_table=1
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98.5%; Pred. No. 1.8e-109;
live 0; Mismatches 11;
'note="ORFID:MW1957"
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/gene="MW1958"
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VGGVDPSIKTFTGKAICPNSHDEAVEAIDNRTVRAGHVVVIRYEGEKGGPGNFEMAR
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RTLNNNQPEDVLARRESLTPFKAKVKTGYLARYTALVTSANTGGVMQVPENLI"
7008. 8777
/gene="ilus"
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TLAIANEAGIDYDLERINAIAKRTPYLSKIAPSSSYSMHDVHEAGGVPAIINELMKKD
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protein id="BAB43143.1"
|db_xref="GI:13701851"
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/gene="GA1860"
/note="ORID:SA1860
hypotherical protein, similar to acetolactate synthase
small subunit"
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product="acetolactate synthase large subunit"
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/product="2-isopropylmalate_synthase"
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Pred. No. 1.8e-109;
0; Mismatches 11;
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/gene="leuA"
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/gene="leuA"
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Matches 855;
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Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
Technology; 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan
(E-mail:tohta@sakuta.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13873637.

Location/Qualifiers
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Ohta,T.
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APPO1334 BA000017
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                          /codom_start=1
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FRVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITKVVI
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ASKITVGSKAPYNLKWSKGAYFWAKIDGLGATSATRYGDNRTNYRFDVGQAVYAPGTL
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/db_xref="GI:.4247719"
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Pred. No. 2.9e-109;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SAV1945"
complement (8388. .9119)
/gene="SAV1945"
/note="Bacterlophage phiN315"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SAV1946"
/note="Bacteriophage phiN315"
                                   complement (7682. .8173)
/gene="sak"
/note="Bacteriophage phiN315
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/gene="SAV1946"
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Best Local Similarity 98.4%;
Matches 854; Conservative
                                                                                                                                         SAV1944"
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	AED16750  M Staphylococcus epidermidis ATCC 12228, section 7 of 9 of the complete genome.  AED16750 AED15929 AED16750.1 GI:273316220 Staphylococcus epidermidis ATCC 12228 Staphylococcus epidermidis ATCC 12228 Batchylococcus epidermidis ATCC 12228 AED16750.1 GI:27316220 Staphylococcus epidermidis ATCC 12228 AED16750.1 Staphylococcus.  I (Dases 1 to 300698) Zhangy Y. Ren, S., Li, H., Fu, G., Lu, L., Lu, G., Jia, J., Tu, Y., Qin, Z., Chen, Z. and Men, Y.	FRATURES Shanghai, 250 Bi Bo Road, China Shanghai, 201203, China Location/Qualifiers Source Jorganism="Staphylococcus epidermidis ATCC 12228"  // mol type="genomic DNA" // stref="axon:17628" // db xref="axon:17628" // product="RNA-Tyr" // product="RNA-Tyr" // product="RNA-Tyr" // product="RNA-Tyr" // product="RNA-Tyr" // product="RNA-Tyr" // product="RNA-Asn" // product="RNA-Asn" // product="Stabha-Gal" // RNA // product="Stabha-Gal" // product="Stabha-Gal" // RNA // produ	gene complement(2718, 2831) /locus_tag="SE1755" complement(2718, 2831) /locus_tag="SE1755" /codon_start=1 /transl_table=11 /product="Hypothetical protein" /protein_id="AAO05396.1" /db xxef="612.27316221" /translation="MulGGRAFEGRAPLGLPNSDKLRMPINLTWESEHG" complement(3977, 5530) /product="165 xibosomal RNA" complement(3977, 15530) /locus_tag="SE1756" /locus_tag="SE1756" /locus_tag="SE1756" /codon_start=1 /codon_start=1
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Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
Patent: WO 02077272-A 386 03-OCT-2002;
Epigenomics AG, (DE)
   genomic DNA (Homo sapiens)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 ATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAG
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1. 805a
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Sequence 386 from Patent WO02077272.
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                                                                               654 GGTTTCATAAACTGAATCGAT
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                                                                                                         97851 AATATIGAATICTIATACTTATTTTTAAATGTACCTIGTAACATGGGCGGAGAA-T 97793
                                                                                                                                                                       97792 TITCGGTTAGATAAAATACATGTGAACCTTGCTACAAGAAGATGTGCATCAG-AGGAGTG 97734
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                                                                                                                                            TTTCGATTTAATACATTAAATGTGAACCTTGCTACAAGATGTGCGATCAGAAGGAGTG
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                                                                       80 ATTACCGAATITITATACITATITGTITAGAATGAACTITATAACATAGTTGGATAGAGT
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                                      5,
Score 307; DB 1; Length 300698; Pred. No. 1.6e-35; 0; Mismatches 90; Indels 2;
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133 c 126 g 279 t
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Pred. No. 2.2e-19;
0; Mismatches 1;
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ch 32.4%;
11 Similarity 80.6%;
383; Conservative
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Matches 200; Conservative
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Anyalabechi, V. Aoyagia, A. Ayodai, M., Anguiano, D.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalabechi, V., Aoyagia, A., Ayodai, M., Baca, E., Baden, H., Bandaranaike, D., Barber, M., Banstead, M., Benahmed, F.,

Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Eurrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Cencer, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, S., Chen, Y., Chen, C., Cox, C., Duya, M., Cree, A., D'Souza, L.,

Dayla, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Danson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, W.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M.,

Gunzatne, P., Hansla, A., Garcia, A., Garra, M.,

Gunzatne, P., Hasland, W., Hamil, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Hane, P., Hawes, A., Hadenson, N., Hernandez, J.,

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Jackson, L., Jacob, L., Jang, H., Johnson, R., Johnson, R.,

Mandarde, M., Mall, Y., London, P., Longacre, S., Lopez, J.,

Inlu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Inlu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Mandard, W., Mathindartne, M., Mathin, R., Maztinez, E.,

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Pageternak, S., Paul, H., Perez, A., Pal, S., Parks, R.,

Pageternak, S., Paul, H., Perez, A., Pel, S.,
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*** SEQUENCING IN PROGRESS ***,
1014 -----TARARATTATTTTTARARATTATATATATATTTTTATTCATTTAAATAA 961
                                                                                                             586 ACGATAACAATTTAATAACGAAGTTATTTATTCAGCATTGGGACATAAAATTAACTTA 645
                                                                                                                                                                                                                                                                 646 AAATITAAATATIGAAGAIGCITITAAITAAAGITAAAGACCAGCCATACCITATITICAGC 705
                                                                                                                                                                                                                                                                                                                               TTATTAAGCTTGACACAAGGTACACTAGTCTTTTTATTTTTAATATTTTCTTAGAAAATCA 765
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                       AC125567
AC125567.5 GI:24817949
HTG; HTGS_PHASE1; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Submitted (29-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

CE 3 (bases 1 to 170627)

Rat Genome Sequencing Consortium.

S. Rat Genome Sequencing Consortium.

Direct Submission

AL Submitted (09-MOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2002 this sequence version replaced gi:23096537.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome contigs are confered, and separated in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence only contigs will be indicated in the feature table.
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shetty, J., Shvartsbeyn, A., Sisson, T., Sitter, C.D., Smajs, D., Sneetty, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sora, J., Steimle, M., Strong, R., Sutton, A., Sovetek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thogey, A., Trejos, Z., Usmani, K., Vales, R., Vera, V., Villasana, D., Waldrow, L., Walker, B., Wang, J., Walliams, G., Wailson, S., Warren, R., Wei, K., Wooden, H., Worley, R., Wright, D., Warlet, R., Wu, J., Yakub, S., Yen, J., Yoon, V., Weight, D., Watsh, R., Wu, J., Zaho, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Folt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: pgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GDDV
Center clone name: GDDV
Consensus quality: 16492 bases at least Q30
Consensus quality: 165269 bases at least Q30
Consensu
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NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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Center: Baylor College of Medicine
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Unpublished
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COMMENT

equip of 109158 bp in length gap of unknown length contig of 1022 bp in length gap of unknown length contig of 1160 bp in length gap of unknown length

109258: 0 110258: 0 110380: 0 111540: 0

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                                                                                                                                                                                                            Length 170627;
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 170627: contig of 58987 bp in length.
                                                                                                                                                                                                                       Similarity 48.2%; Fred. No. 6.1e-05;
11; Conservative 0; Mismatches 312; Indels
                                                                                                                                                                                                            DB 2;
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Pred. No. 6.1e-05;
                                  organism="Rattus norvegicus"
                                                                                                                                                               end_sequence:BH341988"
. 30081 c 30017 g 54086 t
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1 1284
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3636. .4924
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            Location/Qualifiers
1. .170627
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INV 29-JAN-2003

linear

Plasmodium falciparum 67970 bp DNA AL031746 AL844501 AL031746.9 GI:6594243 ·

PFMAL1P3 LOCUS DEFINITION ACCESSION VERSION

RESULT 10

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Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, T. Christodoulou, Z., Clark, R., Corton, C. Cronin, A., Davies, R., Davis, P., Dear, P., Learch, F. Hamlin, N., Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holmson, D., Karpornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Line, A., Maddison, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Sutherford, K.M., Sanders, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 house, and nother of the streps.
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Gene="FrA655c"
| Agene="FrA655c"
| Agene="FrA655c"
| Anctes | Agene | Agene
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The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PFA0580c"
/note="Originally annotated as Plasmodium falciparum;
conserved hypothetical protein but pfam match and other
evidences suggest that it is a putative deoxyribonuclease;
earlier start site possible to make a 412 aa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris, B.
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CBIO 1SA, UK.
CBIO 1SA, UK.
On Dec 16, 1999 this sequence version replaced gi:5763807.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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complement(join(1392..1461,1752..2598,2748..2848)
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Barris, D., Lawson, D., Quail, M., Rajandream, M., Hall, N. and
Barrell, Burrell
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Plasmodium falciparum 3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (join(201. .257,455./gene="PFA0575c" /note="synonym: MALIP3.01b"
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/isolate="3D7"
/db xref="taxon:36329"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .67970
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Best Local Simi:
Matches 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="MA11P3.02"
/gene="MA11P3.02"
/note="contains possible signal sequence. Signal peptide
predicted Signal 2.0 HMM (Signal peptide probabilty
0.640, signal anchor probability 0.357) with cleavage site
probability 0.504 between residues 27 and 28. ScanRegExp
hit to PS00867, Carbamoyl-phosphate synthase subdomain
Pfam match to entry PF01026 TatD DNase, TatD related DNase, score 117.30, E-value 2.9e-31 Similar to plasmodium faliciparum conserved hypothetical protein, upf0006 family mallp3 01 SWALL:0900N6 (EMBL:AL031746) (412 aa) fasta scores: E(): 3.7e-150, 100% id in 412 aa, and to Saccharcmyces cerevisiae putative decxyribonuclease yb1055c yb1055c or yb10512 or yb10511 SWALL:RBFS YEAST (SWALL:P34220) (418 aa) fasta scores: E(): 2.5e-19, 30.47% id in 397 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MTTYKENVGISNKGNKKKKSCQNISFLNFLSFDWIRPLINDLIK
BODGELDNICNRPDVPYASKLEENLENDIEUDSDEFVSEKNSGNEHVLHCNSNDASE
KKVYNYYYHNILMSILKTFKRRIILIISFYILETLIVTLGKFIDYYRKILEGQKIPV
YISFLKDFKVFSGLVVVMIMFPHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NHLOMPDAFYNTYRKFSSQTEIDEISRDFLSIGKNASSSSGIKNNKNIDIDNNKFVEN
DYIINFIKSTKKMEKDSLNERRSLPNVNIYNIMFSDVPSVTFFVTSCINLENVEVKIF
REFYUHRIKGSNSVGIAIMLSIALVSAMILEBELSBLFKKYKYKITKRDKRIDNMHHVL
KEFKLIKMFWMESPERYINIPERKENKYCKRILYLSNIGVFISSISBDIVEVVIFFI
YLKDRINKKEEIKFTSIMPLYVYKILLISNVANFPNIVNNWMEGIVNIKRLINDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB63557.1"
/db_xref="G1:6594245"
/db_xref="SPTREMBL:09U0N5"
/tanslation="WKLINNRFVVLCPIIILFFFLNSVVLGNNNRNNINFHETENAAK
AMRKLLSGEINSIKLDNGDELKIKLNDEKHKOSTKWDKSYSFISNLEBEKYSGTDLFR
KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEKDKEYLENLKYKIIKŶPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
LYMPELHMROSETFFKYUDIYKELFERKOGVLHEFDKEDIVHIIVQNYKNLYIGVNG
CSIKSLENINAVKKI PLINLLLENDAPWCGYKKTHASYEYIKOTYEKRAYTNLKKIKN
IIKCDDNTIFKERNEPYNIADIAEIIYKVREEAVPFDLFCKK"
                                                                                                                                                                                                                                                                                                                              'product="Tatb-like deoxyribonuclease, putative"
'product="Tatb-11ke deoxyribonuclease, putative"
'procein id="CAD49106.1"
'db_xref="Gi:22447010"
'translation="MKIVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOTKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKWFDGVYNSKKHENDLQNVLNRAK
NNNVDKIIITCTCLAEIDKSLKICETYDPGGKFLYLSAGVHPTNCYEFIDKNKHEEKE
IIAKKEYEEFIKYFKNEQVENSKMENGNKKICDGEKDMNLNEILLEKNLDTIPGFKY
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Similar to Schizosaccharomyces pombe ATP-binding cassette
transporter abcl abcl or spac9e9.12C SWALL:ABCL_SCHPO
(SWALL:092337) (1427 aa) fasta scores: E(): 4.2e-08,
21.46% id in 1146 aa"
/codon_start=1
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/note="Putative ABC transporter
Pfam match to entry PF00005 ABC tran, ABC transporter,
score 45.00, E-value 1.7e-09; HMMSmart hit to SM0382,
ATPases associated with a variety of cellular activities;
ScanRegExp hit to PS00211, ABC transporters family
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/protein id=CAB63588.1"
/db_xref="GI:6594246"
/db_xref="GOA:09U0N4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3179. .10303
/note="Putative centromere"
14884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GOA:Q9UUN4"
/db_xref="SPTREMBL:Q9UON4"
/db_xref="sPTREMBL:Q9UON4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="synonym: PFA0590w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="synonym: PFA0585w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="MAL1P3.03"
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gene="MAL1P3.02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKRNSLAIIIGNVGSGKSAFFHSILGDFNMTHGNLYIENFFKKMPILYVPQNSWLFMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="18s ribosomal RNA A-type"
/note="18s rRNA exppressed in asexual stage parasites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="ITS1 A-type"
/note="ribosomal operon internal transcribed spacer 1
expressed in asexual stage parasites"
26439. .26559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 AAAATAAAAAATATCAATAAGTTGGAGTCATTACCGAATTTTTATACTTATTTGTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AATGAACTITATAACATAGTTGGATAGAGTTTTCGATTTAATACATTAAATGTGAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 GCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATAATGAGTAAAATTAATGATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 AIGAITIAGICAACGCAACAITICAAGITAAGAAGITITICAGAGAIACAAAAAAAGAAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="28s rRNA expressed during asexual development"
complement(join(31966. .32476,32675. .32775))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Incte="ribosomal operon internal transcribed spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="mall_5.8srNA"
product="5.8s ribosomal RNA"
/note="5.8s ribosomal_exppressed in asexual stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.7%; Score 91.4; DB 3; Length 67970;
ilarity 47.6%; Pred. No. 0.00013;
Conservative 0; Mismatches 396; Indels 13;
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/note="synonym: PPA0610c"
complement(join(31966. .32476,32675. .32775))
/gene="WAL1P3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed in asexual stage parasites" 27436. .31539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA (A-type)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="28s ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26439. .26559
/gene="mal1_5.8srNA"
26439. .265<u>5</u>9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23896. .26044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26045. .26438
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th O	1		gen CDS	gen GDS	Ð.
Db 8688 TAAATTAATAATATAATAATAAATAATATATATATAT	Db 8927 TAÀATAAATAATÀTTAAATAATAATTÀATAATTAATAATA	CTTA   AATT AGTA       AATA	RESULT 11 AF466146 LOCUS DEFINITION Melipona bicolor mitochondrial genome, partial sequence. ACCESSION AF466146 WESSION AF46146 WESSION AF466146 WESSION AF4661	ψ	. 0 / 11

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COMPLEMENT (9377...9655)
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Pred. No. 0.00028;
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Best Local Similarity 47.2%;
Matches 345; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (6339. .7985)
/gene="ND5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6339. .7985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $600. .$665
/product="tRNA-Gly"
$666. .6019
/gene="ND3"
$666. .6019
/gene="ND3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6212. .6278
/product="tRNA-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="tRNA-Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="tRNA-Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="tRNA-Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6273.
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transl_table=9
                                                                                                                                                                                                                                                                                                                                                               4814. .5590
/gene="COIII"
                                                                                                                                                                                                                                                                                                                                                                                                                    814. .5590
gene="COIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="cox3"
                                                        note="ATP6"
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join(322. .603,826. .1023,1197. .1301,1458. .1533,1696. .2942)
gene="MAL3P5.1"
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LLRCFTMKLNIERNNKOTIRSNYDNINDISIDKDMYMNPIDDVINNISLDEKIKEQ
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                                                                                                                                                                                                                                                                                                                                                                   RSPQIYRKRFKRSRIKAVSFKKKQKKPLFLFENLKKGFSFLGFWRNQYDQKYIDDVIS
NINNLTRIKQVTHKKKSNBFTKENIKQILLHCVFSKIDFKIINNLSYIIKHFQMSNIT
VHSILNQISEKVKEKKDAENYLALHLFLLKDENITLFSMMHIMDFFKSKQKVIECIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Signal peptide predicted by SignalP 2.0 HMM (Signal peptide probability 0.635, signal anchor probability 0.287) with cleavage site probability 0.594 between residues 21 and 22; CDS conserved in p. knowlesi and P.yoelii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="MLGLKRKNVFYLLVSVPSLFAYFLKRHKDNENNYETLINNNDIE
KIKKIRIHNKCSYIPLLFLNIYDSYIYKNKILRMLYFKFRKRRKDKEEYYYITUMVRK
KRREAIKYNFISDEQNLFNKFYIYEIVLEYSLKYGILSPHLSLYILKNISEHCVNIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLYYYNKLDNKHNL NEKKLKYFKOLNNEHTOQAPTNHTHHNNNNNKKFLDINIHSC
KNTNISSYSTYNNMEKENINIYDKYNIHNFYTEKSISYKDENCQHITLMNIYLLNQTY
DNICRICLNTNTYIYIYNIYINEKMINILKYICYKNMEIILLNYNHIEDMKKKINQKNNTNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFYXIYSFFFFKKEENHIYDLFEDQMMHLHKKENDKFYNYSNENTHNNIYKYISDNY
YPHINSSENCSFRUCKOTDDNIYHIIMGKEEYPPMKESDBEKKONYTCGNINIEK
DQKKDILKKIYFLKGNYLDDIQILNELYYTYMRLLFECSLKLISIKKNIHLEEKKME
FDKDNKIIYLNSADYMNNLRRNILKRFSKNEERENINSFAŞFPFLLSKNIIYFEDEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YELAKIYTNUI FDYLKGKKEKHQUEDNTINLYYIKKKPWIFYLKNII KUKDTSFIEH
NNNIVNGDIKNNNII FKKKYNLFESSIISYPYIKDIYENYKLRLYYIYDDLKKFCR
YFLKMNEHINRKLYMKRAFHYIYNFDQFIINNYYHIHKKNIHKIHIHLKQCKDKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INEQYPIIKNEKTVLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSRDNTIYNNVYDKETNKTTTNNNNNDNDNICSNNDHICSNNNDHICSNNNDHICSN
NNNNICSNNNNNICSNNNNNICSNNNNNICSNNGMLDEFCQDNKFNDYNTRKKERRRI
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YSYDTWANSFTFSYFFFSLSYLLFILPYHPDMYASYIFFKTLTYSGLPTYYYSLYNNI
MVVGPKT"
join(7669. .7717,7800. .7829,7912. .7940,8064. .8106,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /KNK1 KKYLTYLNNN1 SNDLYPYN1 SYNK1 YNQNKYKNRKNFSH1 FYSLKND1HLLLF
                                                                                        /notes="Possible signal sequence present, revised: added
new exon 2, revised: incorporated new intron in last exon
in comparison with P. knowlesi and P. yoelii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDIVKFKDLYYCMINNINNIFSYIHKVDHNECVYRIFKAYNKILLYEYNYLNEKENIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/protein id="cAB38968.1"
/db_xref="G1:449392"
/db_xref="G1:49392"
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protein_id="CAB90285.1"
db_xref="GI:7711066"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: PFC0580c"
complement(3354..6644)
/gene="MAL3P5.2"
            note="synonym: PFC0575w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (3354, .6644)
/gene="MAL3P5.2"
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/gene="MAL3P5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Bučkec, C.O., Burxows, C., Cherevach, I., Chillingworth, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Cronin, A., Davies, R., Davies, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornby, T., Holroyd, S., Larke, N., Kerbornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Line, A., Maddison, M., Molean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabbinowitsch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M., Squares, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevenes, K., Taylor, K., Tivey, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.
                                                                                                                                                                                                                                                                              INV 29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawson, D., Bowman, S. and Barrell, B.
Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
664 AATAAATTATTCATGAAATGGGAATATTCTTAATTTTAAAAATATATTTAATAAA 605
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ON Oct 2, 2002 this sequence version replaced gi:7711064.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    Plasmodium falciparum MAL3P5, complete sequence.
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179 AL844502
AL034556.4 GI:23477013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete nucleotide seguence of chromosome 3 of Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; centromere; CTRP protein; initiation factor B4;
Serine/threonine protein phosphatase.
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/organism="Plasmodium falciparum 3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 400 (6744), 532-538 (1999)
                                                                                                                                                                                                                                                                          86826 bp
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chromosome="3"
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join(322. .603,8
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PFMAL3P5/c
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KEYWORDS
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TITLE

SOURCE

FEATURES

COMMENT

207

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40854 TAAATTAAAATTAAAAATATAAATGTTATAATTAAATTTAATTAATTAATTAATTAAATTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACCTTACTATTTAAACTTAAAGCTTTACAAAAGCTAAAAGATTTAAAAATTGTTATCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCAGAGATACAAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATATTCAAAAACTGATTTCAGAATTAGAAGAATACATTAAAAATTAAATCAAGGTTAAT
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                                                                                                                                                                                                          ATGAGTAAAATTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAGAAGITTTACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCA
                                                                                                                       TAATACATTAAATGTGAACCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATA
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Complement (join [13653. .1754,18005. .19353))

/note="Mali3F5.4"
/note="Mali3F5.4"
/note="Synonym" PFC0590c"

complement (join [13653. .17754,18005. .19353))

/gene="Mali2F5.4"
/note="Signal peptide predicted by SignalP 2.0 HWM (Signal peptide probabilty 0.921, signal anchor probability 0.075)

with cleavage site probability 0.888 between residues 20 and 2. revised: changed donor in comparison with P. knowlesi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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/product="hypochetical_s"
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/db_xref="SPTREMBL:097275"
/db_xref="SPTR
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INNNNNNNNNNNIYIDINIQFVNKNYSCTHNNVIKNETNDNYPNSTIRNQHPNDQV
ILNNPVFFYNKKLNVVDSIDFEYELFCYNLYLDIYKIVCLKLLTLKNHKLSCLQSID
                                                                                                                                                          ONFLKEERNNSDKLODDIDEDERKYPDEELERRAKKKEEEYDKUDEEL COMPLEMENT (10024. 10044,10320. 10336,10397. 10445, 11613. .10674,10773. .10798,10920. .10399,11157. .11237, 11673. .11515,111715. .11767,11950. .12040))
// Gene "PFCOS82c" complement (join(10024. .10044,10320. .10336,10397. .10445, 11613. .10674,10773. .10798,10920. .103999,11157. .11237, 11453. .11515,11715. .11767,11950. .12040))
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/db_xref="spPrEMBL:Q9NFA3"
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GEIWRLFTPYLYIGNLYLQYILMFNYLNIYMSSVEISHYKKPEDFLIFLTFGYISNLL
FTIWANMYNENIMNVKLYIHNFKNFFIKDCVSKYTSRSSTNNNSNNINSNNRSSNNNN
                                                NDI KTTVTAMKNKMDQLLTTSYSNKKI DTVNASFQWAQSPEYI FLNI KFSHRWSSPGA
LKVKDEEI VSKKNNFSFSALSNDSNSVTKKYI VDLTLLDNI IESETKYNFASVGKVVV
TLKKEKKKI WNRLLLSKEKY PNMQVWWDMKEKRIHI I TFVTINLFFLLSLSHRYHDSV
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DMTKKYKEGVDFLKESERRAQDIEDIGYTIMSELNSQRSAILRTKHHTDETRQEQNRV
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LTFINYNINBSIQIIKLIGMLISVHKHNKLSPPHMNLNVQNAANYLFKNLYNLQNI
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             QKIFHIYFANEQIASSFFESHKNYRVTKEDIIDGIEKCWFNITDYLISESIKQDNDFS
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larity 46.7%; Pred. No. 0.00017;
Conservative 0; Mismatches 441; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Revised: new gene prediction"
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PAT 14-FEB-2003
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           linear
AX599046 8056 bp DNA Sequence 386 from Patent WO02077272. AX599046
                                                                                        AX599046.1 GI:28399186
                                                                                                                                          synthetic construct
synthetic construct
artificial sequences.
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AUTHORS
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41034 AATAATAATTTAAATAAATATATAATAATAATAATTAACTATATATATATATATAAAATAA 40975

AAAAGTTATTGGGCATTTTTTGAAAATAAAAAATATCAATAAGTTGGAGTCATTACCGA

Similarity

Best Local Sim Matches 395;

Query Match

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ATTITIATACTTATTICTTTAGAATGAACTTTATAACATAGTTGGATAGAGTTTTCGATT 147

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/mol_type="genomic DNA"

/db xref="texon:32630"

/note="chemically treated genomic DNA (Homo sapiens)"

- 0 c 371 g 3974 t
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                                                                                                                                            Length 8056;
                                                                                                                                            9.5%; Score 90; DB 6; Length 805
46.0%; Pred. No. 0.00041;
tive 0; Mismatches 400; Indels
       WO 02077272-A 386 03-OCT-2002;
Patent: WO Ozurra
Epigenomics AG (DE)
Location/Qualifiers
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AE014832 258658 bp DNA linear INV 07-OCT-2002 Plasmodium falciparum 3D7 chromosome 10 section 4 of 7 of the complete sequence.

LOCUS DEFINITION

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Barrell,B.
Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
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YSTLDFTROAGSVITARNFNHNGKNDPINNKILLETUBSFDELLEPYTEGDEDTITFPG
RQHHKWNDGCYPUNKKKCNNKLKKERKNNSYLFKKEDKITKKCIHIIKNNSRQNDFNNYN
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DFDLDIPEYFWNKYPSHAMPEIYKYMEIPERKKTCIIEKETIGSMMNYSSIIINVNAVQ
PYTYRIVMLLEFIHVLALLLNDFLFV
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SHYRKRYKKKKKKMDLGYKNKINDNYKYKEMKMAIKKEYIKEDDMQYNDRKYYDLANK
KDISFLLSYSDNDIYRNHKYYYNLEKYTDPKLEPFENINNLTTNINNKKYYONITN
EYVSHNNYNDITEDEBNKVIKINMAPIYHSTNPSSYTTYNNLFSIKLLCHAKCYNLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (13-SEP-2002) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
Location/Qualifiers
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Methods and nucleic acids for the analysis of hematopoietic cell
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Patent: WO 02077272-A 240 03-OCT-2002;
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Sequence 240 from Patent WO02077272.
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are included to maintain the nucleotide numbering
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Maximum Match 100%
Listing first 45 summaries
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Minimum I Maximum I

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Searched:

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Scoring table:

us-10-043-539a-1.rng

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can also be used in a kit for the immunodetection of Saureus in a sample. Staureus in fection. The polypeptides can also be used in a kit for the immunodetection of Saureus in a sample. Staureus in a sample, stareus in a sample starensist in the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used for their fragments) are useful as primers or probes for isolating computer readable medium.
                                                                                                                                                                            rolynucleotide(s) and proteins derived from stored on computer readable medium and used anti-S.aureus vaccines
                                                                                                                                                                                                                                                                   Claim 1; Page 1984-1985; 3271pp; English
                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                             WPI; 1997-374922/35.
                                                                                  Barash SC,
                                                                                                      Rosen CA;
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Staphylococcus aureus in the production of

Kunsch CA

Fannon MR,

Dillon PJ,

Choi GH,

96US-0009861

05-JAN-1996;

Sequence 400 BP; 155 A; 36 C; 44 G; 104 T; 61 other;

274 GATACAAAAAGAAGTICAATTIGAACTATGAAGAAATTTATATTTTAAATCATATTTTA Gaps .. 0 34.7%; Score 329; DB 18; Length 400; llarity 84.4%; Pred. No. 2.2e-46; Conservative 0; Mismatches 61; Indels ( al Similarity 329; Conserv Query Match Local Matches ò

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333 393 120 453 180 9 GATACAAAAAGAAGTICAATITIGAACTATGAAGAAATTTATATTTTAAATCATATTTTA TACTATITAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAAATTGTTATCAAAGAAAAGA AGAAGTGAGTCTAACGAAATCTCATCTAAAGAGATTTGCTAAGTGCTCAGAGTTCAAACCT AGAAGTGAGTCTAACGNAATCTCATCTAAAGAGATTTGCTAAGTGCTCAGAGTTCAAACCT TACTATTTAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAGA 334 61 394 121 g ò d ò g

AGTITACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATT CAAAAAACTGATTTCAGAATTAGAAGAATACATTAAAAATTAAATCAAGGTTAATTGCGTT 241 CAAAAACTGATTTCAGAATTAGAAGAATACATTAAAATTAAATCAAGGTTAATTGCGTT AGTITACAAGACGAAAGAACAGTIATTGTTTATGTTACAGATACACAAAAAGCAAATATT 454 181 514 ò 셤 ò 유

240 513

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AAAATTAACTTAAAATTTAAATATTGAAGA 390 AAAATTAACTTAAAATTTAAATATTGAAGA

ABN92693 standard; DNA; 387 RESULT 2
ABN92693
ID ABN9

epidermidis; open reading frame; ORF; bacterial infection; ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP3124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis lifection. When The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site. Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2156 Sequence 387 BP; 175 A; 39 C; 55 G; 118 T; 0 other; Disclosure; SEQ ID 2156; 267pp; English. gene; ds. THERAPEUTICS CORP gene therapy; 97US-055779P. 97US-064964P. 98US-0134001 ä Staphylococcus epidermidis (first entry) Bush 2002-381255/41. Doucette-Stamm LA, P-PSDB; ABP40148 Staphylococcus antibacterial; (GENO:) GENOME 24-JUL-2002 13-AUG-1998; 14-AUG-1997; 08-NOV-1997; US6380370-B1 30-APR-2002 

1; Gaps DB 24; Length 387; Indels Query Match 27.6%; Score 261.4; DB 24; Best Local Similarity 81.4%; Pred. No. 4.2e-35; Matches 315; Conservative 0; Mismatches 71;

1;

284 CATCAATGATTTGGTTAATGCGACATTTCAAGTAAAAAATTTTTTTAGAGATACTAAAAA 119 344 TAACGAAATCTCAATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACTATTTAAC 404 239 464 9 165 ACCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGTTTTAATAATGAGTAAATTAATGA TAACGAAATATCTTCAAAAGAAATTGCTACATGTTCAGAGTTTAAACCGTATTATTTAAC 1 ACCTTGCTACAACAAGATGTGCATCAG-AGGAGTGGTTTTTATAATGGGAAAAATTAAAGA 225 TATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAA GAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAAATCATATTTTAAGAAGTGAGTC GCAATATAATTTAAATTATGAAGAAATTTATATTCTTAATCACATTTTGAAAAGTGAATC TAAAGCATTACAAAAATTAAAAGATTTAAATTTACTATCTAAAAAGAGAGGGTGCATGA TAAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAGAAGTTTACAAGA 09 285 120 345 180 405 240 ò d Op g ð ઠે qq  $\stackrel{>}{\circ}$ ð 임

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                        Haematopoietic cell proliferation disorder related DNA sequence #386.
                                                                                                                                                                                                                                                                     Human, haematopoietic cell proliferation disorder, cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Braun A, Distler J, Guetig D, Howe A, Mueller J; Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B; Lipscher E, Maier S, Model F, Mueller V, Otto T; Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 other;
                                         360 TTTAGAATTAGAAAACTATATCAAATA 386
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                TTCAGAATTAGAAGAATACATTAAAAA
                                                                                              RESULT 3
ABZ10246/C
ID ABZ10246 standard; DNA; 8056
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                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG.
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Pelet C,
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Score 96.2; DB 25; Length 8056; Pred. No. 1.4e-07;

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Query Match Best Local Similarity

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G, Lesche R, Leu E;
Mueller V, Otto T;
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9.5%; Score 90; DB 25; Length 80
Best Local Similarity 46.0%; Pred. No. 1.6e-06;
Matches 341; Conservative 0; Mismatches 400; Indels
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                                                                                                                                                                                                                            , Braun A, Distler J, Guetig D, Piepenbrock C, Adorjan P, Grabs Lipscher E, Maier S, Model F, Schwope I, Ziebarth H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 28; SEQ ID 386; 117pp; English.
                                                                                                            26-MAR-2002; 2002WO-EP03401.
                                                                                                                                                    26-MAR-2001; 2001US-278333P.
                                                                                                                                                                                      (EPIG-) EPIGENOMICS
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Lewin A,
Pelet C,
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Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG Haematopoietic cell proliferation disorder related DNA sequence #240. Mueller J; Human, haematopoietic cell proliferation disorder, cytostatic; gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia; cytosine methylation state; gene; ds. G, Lesche R, Le Mueller V, Otto

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The present invention describes a method for detecting and differentiating between haematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated cipd CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 copresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related supplication of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subject subjects cell proliferation disorder related becauseds, present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method canables a highly specific classification of haematopoietic cell proliferative disorders cell proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 other;
SEQ ID 240; 117pp; English
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947 TAAATITITITITITITIAAACGAATAAAATAAATATTATAATITITITITITITAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sednences
of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, tumour suppressor gene, oncogene, antitumour, cytostatic, cancer, tumour, CpG dinucleotide, single-nucleotide polymorphism, SNP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically presereated DNA (CP DNA) e.g. with obsulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequence (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
                                                                       827 AAATAITITITAAAAAAAATCGITITITITIATITITITITACGIATAAAATITICGIA
                                     745 TAATATTTTCTTAGAAAATCAAGTTTACGATCATAAATATTTTCTGCGATATAGCTTTGG
                                                                                                       ATGGTTCCAAGTATTTTCTCTATAATTTGTGTGCGATAAGCAAAAATTCTAACTGCAAAA
                                                                                                                                           ATTATTTAAATTTTATATTTAATTATTTTCGTCGTTTTTCCTAATAAATTTTTTTAAAAA
                                                                                                                                                                           865 CCATGTGTAGGCAATTGAGAAATAGCAACACGACAATCGGATGTATTGCTATAAGAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour suppressor gene derived chemically modified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 459; 27pp; English.
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20000E-1019173.
20000E-1032529.
20000E-1043826.
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cytosine methylation; ds.
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30-JUN-2000;
01-SEP-2000;
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(first entry)

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Human, haematopoietic cell proliferation disorder, cytostatic, gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia, cytosine methylation state, gene; ds.
                                                                  Haematopoietic cell proliferation disorder related DNA sequence
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Pelet C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3472 ААССААААААААААААААААСАССАТААААСАСАТАТТТТАААТТААТТААТТААТТААТТААТТААТТААТТА
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diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                          50 AAAATAAAAAATATCAATAAGTTGGAGTCATTACCGAATTTTTATACTTATTGTTTAG
                                                                                                                                                                                                                                                                            110 AATGAACTITATAACATAGTTGGATAGAGTTTTCGATTTAATACATTAAATGTGAACCTT
                                                                                                                                                                                                                                                                                                     170 GCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATAATGAGTAAATTAATGATATTA
                                                                                                                                                                                                                                                                                                                                                         290 TCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTTAAGAAGTGAGTCTAACG
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                                                      genomic sequences derived from tumour suppressor genes and
                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                        Length 6292;
                                                                                                                                                                       Score 82; DB 22; Length 62
Pred. No. 3.4e-05;
0; Mismatches 410; Indels
                                                                                                                                               Sequence 6292 BP; 1736 A; 99 C; 1304 G; 3153 T; 0 other;
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45.9%;
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Best Local Similarity 45.9
Matches 350; Conservative
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Mueller'J; e R, Leu E; , Otto T;

Howe A, Muells G, Lesche R, Mueller V, Ott

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in given. Inventor describes a method for detecting and associated with at least 1 gene and/or their regulatory regions in a seociated with at least 1 gene and/or their regulatory regions in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZO9861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative discorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferation of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders.
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Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG
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                                                                                                                                                                                                                                                                                                                                                                          present invention describes a method for detecting and
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45.5%; Pred. No. 6.7e-05;
tive 0; Mismatches 433;
                                                                                                                                                                                                                                                                 Claim 28; SEQ ID 240; 117pp; English.
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Matches 368; Conservative
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ВЪ

standard; DNA; 8056

ABZ10100 ABZ10100/c ID ABZ101 RESULT 7

96US-0009861

05-JAN-1996;

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                         1373 ATTTTTAÄTAÄAÄATTTAAAATTTÄÄÄTTTTTTTTTTÄÄÄÄÄTTÄÄÄÄÄTÄÄÄTTTTT 1314
                                                                                                                                          <u> ATTTTÄAAATTÄAATTÄATAATAATCGAAAATATATTAATTTTAAATTTTCGAATATCGAA 1134</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAAATAAAATTTATTTTAAAAAATTTTACGAAAACGACGAAAATAATTAAAATA 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u> AAATTTTAAATATTGAAGATGCTTTAATTAAAGTTTAAAGACCAGCCATACCTTATTTCAGC</u>
                                                                                                                                                                      AACGAAATCTCATAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACTATTTAACT
                                                      ATTAATGATTTAGTCAACGCAACATTTTCAAGTTAAGAAGTTTTTTCAGAGATACAAAAAG
                                                                                  AAAGCTTTACAAAAGCTAAAAAGATTTAAAAATTGTTATCAAAGAAAAAAAGAAGTTTACAAGAC
                                                                                                                                                                                                                                                                                      GAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATTCAAAAACTGATT
                                                                                                                                                                                                                                                                                                                .073 CGAAATTTTTTTTTTACGTAATTAAATTTCGAAATTAAAAAATAAAAAATTTT-
                                                                                                                                                                                                                                                                                                                                                                                                      ACGATAACAATTTATTAATACGAAGTTATTTATTCAGCATTGGGACATAAAATTAACTTA
CCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATAATGAGTAAAATTAATGAT
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelial infections, food poisoning, osteomyelitis, shin and surgical wound infections, scaled skin syndrome, otc. Organisms transformed with the DNA sequences can be used for the transment production of the polypeptides. The new DNA sequences can be used and their fragments) are useful as primers or probes for isolating the new companion and the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epidermidis; open reading frame; ORF; bacterial infection; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 ACTIATITICITIAGAAIGAACTITAIAACAIAGITIGGAIAGAGITITICGAITITAAIACAI
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                                                                                                                                Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79.4; DB 18;
Pred. No. 9.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 101 BP; 33 A; 20 C; 12 G; 35 T; 1 other;
                                                             Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                         English.
                                                             Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%;
                             (HUMA-) HUMAN GENOME SCI INC.
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97US-064964P.
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                                                                                                                                                                                                         Claim 1; Page 2007; 3271pp;
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                                                           Choi GH,
                                                                                                          WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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ID ABN92692
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                                                                                Rosen
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Matches
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences an also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life Cycle or Inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site 

Sequence 867 BP; 309 A; 146 C; 140 G; 272 T; 0 other;

ö 748 803 808 863 864 ACCATGTGGGCAATTGAGAAATAGCAACACGACAATCGGATGTATTGCTATAAGAACT 923 744 ITAATATITITCITAGAAAATCAAGTITACGATCATAAATATITITCIGCGATATAGCTITG 867 TIAATATITICITAAGAAGITAATITIGICGATGATAAATCGITIGATATATGATITG 807 AACACGAGTCAAAATTTCTTCTATTATTTGAGTTCTTTTAGTCAAAATACGAACGGCCAA 804 GATGGTTCCAAGTATTTTCTCTATAATTTGTGTGCGATAAGCAAAAATTCTAACTGCAAA Gaps . 0 Score 77.6; DB 24; Length 867; Pred. No. 0.00019; 0; Mismatches 79; Indels 0; 79; 924 AATGGTTTCATAAACTGAATCGAT 947 687 AACCGCGTGTAAATATCTTCTAT 8.2%; Query Match
Best Local Similarity 61.3
Matches 125, Conservative Db. Db 셤 ò ò ò 8

RESULT 10

AAA66121 standard; DNA; 529

BP.

AAA66121;

(first entry) 05-OCT-2000

E. coli proliferation inhibiting clone SEQ ID NO:468.

Escherichia coli, E. coli, proliferation, inhibition, screening, antimicrobial, bacterial growth, antisense therapy, antibacterial; ds.

Escherichia coli.

WO200044906-A2.

03-AUG-2000

27-JAN-2000; 2000WO-US02200.

99US-0117405, 27-JAN-1999;

(ELIT-) ELITRA PHARM INC

Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Zyskind J,

Bischoff F, Heinz E, Drexler H, Scheffler J;

Lerchl J, Duwenig E,

WPI; 2002-675961/73

Carr GJ;

AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide agequences derived from Escherichia coli which inhibit E. coli prollieration. AAA65890 to AAA66055 and AAB15886 to AAB16040 represent nucleotide and protein sequences associated with E. coli prollieration. AAA66057 represent primers used for sequencing E. coli prollieration inhibiting nucleotide inserts in an example from the present invention. Methods from the present invention can be used to latentify a prollieration-required gene in a microorganism, by contacting a microorganism with a prollieration-required gene activity inhibitory nucleic acid identified in another organism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and prollieration, can be used for antisense therapy for killing bacteria. 120 Promoter; expression cassette; structural gene; plant; transgenic; linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic; animal nutrition; human nutrition; pharmaceutical; cholesterol; blood; ATATCAATAAGTTGGAGTCATTACCGAATTTTTATACTTATTTGTTTAGAATGAACTTTA 1 GTTTTCAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGCATTTTTTGAAAATAAAAA 377 Gricicaaaarceereeaegecrecareacaaercarceeeeerrarcreaacaraaaaca 317 CTATCAATAAGTTGGAGTCATTACCGACATTAAAAGTAACTTTTTTGAAATTAGAGATAA Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -Gaps . Score 75.6; DB 21; Length 529; Pred. No. 0.00041; 0; Mismatches 29; Indels 0 pUC19 promoter-terminator expression cassette SEQ ID 20. Sequence 529 BP; 140 A; 105 C; 102 G; 182 T; 0 other; Claim 1; Page 313; 316pp; English. ABQ76793 standard; DNA; 12079 BP. disease; seed-specific; ds. 8.0%; 19-JAN-2001; 2001DE-1002338. 19-JAN-2001; 2001DE-1002338. (first entry) Query Match Best Local Similarity 76.2 \*\*\* Ares 93; Conservative Ξ, WPI; 2000-514822/46. (BADI ) BASF PLANT TA 122 TA 256 DE10102338-AI Yamamoto RT, 25-MAR-2003 25-JUL-2002 Synthetic 121 257 ABQ76793 RESULT 11 ABQ76793/ ð Db à d ò g

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This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (LI-P-SG-L2) in where L1 = is a polylinker sequences reproduced (ABG/7612) in where L1 = is a polylinker sequences reproduced (ABG/789-ABG/7801) or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a mon-libration incleic acid in the vector. Transgenic plant esters with an increased content of polyunsaturated fatty acids (PUFA); useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. provide increased and more nutrition, cosmetics and pharmaceuticals, e.g. provide increased and more produce increased and more produce increased and more and more negligible production of fine chemicals, e.g. provide increased and more negligible production of fine chemicals of the invention feared in production of fine chemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GITCTCAAAATCGGTGGAGCTGCATGACAAAGTCATCGGGCATTATCTGAACATAAAACA.3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic; animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTTTTCAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGCATTTTTTGAAAAAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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                         New expression cassette for plant genes, useful for preparing transgenic plants that have increased production of polyunsaturated fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length 12079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12079 BP; 2835 A; 3149 C; 3385 G; 2710 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3689 czarcanakacircarcarraccaninarchia 3654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 75.2; DB 24
Pred. No. 0.00045;
0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant specific expression vector SEQ ID NO 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domerque F,
                                                                                                                                                                         Example 13; Page 112-121; 188pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-2001; 2001DE-1002337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 86.5
les 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-644810/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE10102337-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lerchl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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ID ABV7427

X AC ABV7427

XX ABV7427

XX BY BE Plant 8

XX PL BE Plant 8

XX PL BE PLANT 8

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The invention relates to preparing (M1) fatty acid esters (I) with anomoreased content of polyunsaturated fatty acids (II) with at least two double bonds by introducing into a (I) -producing organism a specific nucleic acid (A) (M1) is useful for preparing ester containing to polyunsaturated fatty acids. Oils, lipids and (II) or their fractions, produced by (M1) are used in animal and human nutrition, cosmetics and pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in the blood and to protect against heart disease. Calls that express (A) are also used to identify (ant)agonists of desaturases, e.g. for modularing the yield and rate of production of particular fine chemicals in microorganisms (claimed). Also (A) and derived proteins can be used as markers of specific genomic regions and in evolutionary/protein structural studies. (M1) is suitable for large scale production (no known bioengineering method can produce (II) on a useful scale). The present promoter and terminator surrounding the site for insertion of an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3749 Gircicaaairdegiedagciedaidacaaadicairdegcairaicidaacaiaaaca 3690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promoter; expression cassette; structural gene; plant; transgenic; linesed; fetty acid ester; polyunsaturated fatty acid; PUPA; cosmetic; animal nutrition; human nutrition; pharmaceutical; cholesterol; blood; heart disease; seed-specific; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scheffler J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GITITICAAAATCGGIGGAGGIGCAIGAAAAAGITAITGGGGCAITITITIGAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preparing
polyunsaturated
                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 75.2; DB 24; Length 12079; 86.5%; Pred, No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drexler H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pUC19 promoter-terminator expression cassette SEQ ID 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New expression cassette for plant genes, useful for transgenic plants that have increased production of fatty acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 13; Page 104-112; 188pp; German
                                  Example 11; Page 108-117; 182pp; German.
gene from Phaeodactylum tricornutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bischoff F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ76792 standard; DNA; 12085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-2001; 2001DE-1002338.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-675961/73.
                                                                                                                                                                                                                                                                                                                                                        expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE10102338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ76792;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ76792/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
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This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SQ) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (LI-P-SG-L2) in where il = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker sequences and n = 1-3. The invention discloses a vector containing sequences and n = 1-3. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a (non-)functional nucleic acid in the vector. Transgenic plants e.g. linseed can be prepared with improved production of fatty acid setul in animal and human nutrition, cosmetics and pharmaceuticals, e.g. UVFA are known to reduce levels of cholesterol in the blood and to provide increased and more efficient production of fine chemicals (especially PUFA), including seed specific production. This sequence increasents a nucleic acid sequence used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
X88888888888888888888888888888888888
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Sequence 12085 BP; 2838 A; 3149 C; 3385 G; 2713 T; 0 other;

0 3749 GTTCTCAAAATCGGTGGAGCTGCATGACAAGTCATCGGGCATTATCTGAACATAAAACA 3690 9 1 GITITICAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGCCATTTTTTGAAAATAAAAA DB 24; Length 12085; ô 13; Indels 3689 CTATCAATAAGTIGGAGTCATTACCCAATTAIGATA 3654 61 ATATCAATAAGTIGGAGTCATTACCGAATTITTATA 96 7.9%; Score 75.2; DB 2486.5%; Pred. No. 0.00045. Local Similarity 86.5 les 83; Conservative Query Match Best Loc Matches qq 8 ò 엄

ABV74270 standard; DNA; 12085 

ABV74270;

(first entry) 28-MAR-2003

Plant specific expression vector SEQ ID NO 21.

Desaturase, fatty acid, ester, polyunsaturated fatty acid, cosmetic, animal nutrition, pharmaceutical, cholesterol, heart disease, transgenic, plant, ds.

Synthetic

DE10102337-A1

25-JUL-2002

19-JAN-2001; 2001DE-1002337,

19-JAN-2001; 2001DE:1002337.

(BADI ) BASF PLANT SCI GMBH

Preparing ester containing polyunsaturated fatty acids, useful e.g. animal or human nutrition, by transforming organism with desaturase animal or human nutrition, by transfe gene from Phaeodactylum tricornutum WPI; 2002-644810/70.

Zaehringer U;

Domergue F,

Heinz E,

Renz A,

<del>ر</del>ا ر

Lerchl

Example 11; Page 100-108; 182pp; German.

The invention relates to preparing (M1) fatty acid esters (I) with an increased content of polyunsaturated fatty acids (II) with at least two

double bonds by introducing into a (I)-producing organism a specific nucleic acid (A). (M1) is useful for preparing ester containing polyumsaturated fatty acids. Oils, lipids and (II) or their fractions, produced by (M1) are used in animal and human nutrition, cosmetics and pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in the blood and to protect against heart disease. (Cells that express (A) are also used to identify (ant) agoinst heart disease. (Cells that express (A) modulating the yield and rate of production of particular fine chemicals in microorganisms (claimed). Also (A) and derived proteins can be used as markers of specific genomic regions and in evolutionary/protein structural studies. (M1) is suitable for large scale production (no known bioengineering method can produce (II) on a useful scale). The present sequence is that of a pucil abased expression vector with a plant specific promoter and terminator surrounding the site for insertion of an expression cassette 

Sequence 12085 BP; 2838 A; 3149 C; 3385 G; 2713 T; 0 other;

Gaps . 0 Length 12085; 13; Indels 7.9%; Score 75.2; DB 24; 86.5%; Pred. No. 0.00045; . ative 0; Mismatches 13; Local Similarity 86.5 nes 83; Conservative Query Match

. 0

3749 GITCICAAAAICGGIGGAGCIGCAIGACAAGICAICGGGCAIIAICIGAACAIAAACA 3690 1 GITITICAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGCCATTTTTTGAAAATAAAAA 61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATA 96 В ठ ò

3689 CTATCAATAAGTTGGAGTCATTACCCAATTATGATA 3654

ద

RESULT 15 ABQ76791/c

ABQ76791 standard; DNA; 12093

ABQ76791;

(first entry) 25-MAR-2003 pUC19 promoter-terminator expression cassette SEQ ID 18.

Promoter; expression cassette; structural gene; plant; transgenic; linseed; fatty acid ester; polyunsaturated fatty acid; PUPA; cosmetic; animal nutrition; human nutrition; pharmaceutical; cholesterol; blood; heart disease; seed-specific, ds.

Synthetic

DE10102338-A1

25-JUL-2002

19-JAN-2001; 2001DE-1002338. 

19-JAN-2001; 2001DE-1002338.

(BADI ) BASF PLANT SCI

Scheffler J; Drexler H, New expression cassette for plant genes, useful for transgenic plants that have increased production of Heinz E, Ľ, Bischoff Lerchl J, Duwenig E, WPI; 2002-675961/73.

preparing polyunsaturated

Example 13; Page 95-103; 188pp; German.

fatty acids

끍

This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (Li-5-G-L2) in where Li = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker

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sequences and n = 1-3. The invention discloses a vector containing sequences and n = 1-1. The invention discloses a vector containing this BC, an organism containing the BC or the vector and a transgenic plant containing a fond. Further the vector transgenic plants e.g. linseed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (BUFA). Buff are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression casettes of the invention provide increased and more efficient production of fine chemicals e.g. (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the
sequences reproduced (ABQ76799-ABQ76801) or equivalent RB-site-containing sequences and n = 1-3. The invention discloses a vector containing this
                                                                                                                                                                                                                                                                                                                                                                                             invention.
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Sequence 12093 BP; 2837 A; 3154 C; 3390 G; 2712 T; 0 other;

0; Gaps Query Match 7.9%; Score 75.2; DB 24; Length 12093; Best Local Similarity 86.5%; Pred. No. 0.00045; Matches 83; Conservative 0; Mismatches 13; Indels 0;

3749 GITCTCAAAATCGGIGGAGCIGCAIGAAAAGTCAICGGGCAITAICIGAACAIAAAACA 3690 3689 CTATCAATAAGTTGAAGTCATTACCCAATTATGATA 3654 61 ATATCAATAAGTTGGAGTCATTACCGAATTTTATA 96 δ δ d

Search completed: November 17, 2003, 09:42:18 Job time : 318 secs

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Sequence Sequence Sequence

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Sequence

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Sequence 2155, Application US/09134001C

Parent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICANTON NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 ACCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATAATGAGTAAAATTAATGA
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81.4%; Pred. No. 8.9e-46;
live 0; Mismatches 71;
                                                 US-08-544-332-8
US-09-370-861A-8
US-08-998-416-185
US-08-998-416-786
                                                                                                                                                                                                                                           US-08-107-755A-8
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, ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2156
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Best Local Similarity 81.4
Matches 315, Conservative
US-09-134-001C-2156
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Sequence 2155, Ap
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being printed,
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and is derived by analysis of the total score distribution.
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/cgnZ_6/ptodata/2/ina/5A_COMB.seq:*
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/cgnZ_6/ptodata/2/ina/6B_COMB.seq:*
/cgnZ_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgnZ_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgnZ_6/ptodata/2/ina/Packfiles1.seq:*
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Compugen Ltd.
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US-09-134-001C-2155
US-09-134-001C-2155
US-09-134-14-10
US-09-134-001C-277
US-08-1414-10
US-08-14-14-10
US-08-14-14-10
US-08-14-14-10
US-08-14-16-11
US-08-12-11
US-08-13-11
US-08-13-11
US-08-13-11
US-08-13-11
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                     version 5
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Maximum Match 100%
Listing first 45 summaries
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                     GenCore (c) 1993
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length: 2000000000
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Perfect score:
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RESULT 4
US-09-948-138-4
US-09-948-138-4
US-09-948-138-4
Sequence 4, Application US/09948138
Patent No. 6534695
GENERAL INFORMATION:
APPLICANT: AGRINOMICS, LLC
TITLE OF INVENTION: DEBNTIFICATION AND CHARACTERIZATION OF A DWARF AND LATE FLOWERING
TITLE OF INVENTION: PHENOTYPE (DLF2) IN ARBIDOPSIS
TITLE OF INVENTION: PHENOTYPE (DLF2) IN ARBIDOPSIS
CURRENT APPLICATION NUMBER: US/09/948,138
CURRENT FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENT NOS: 4
LENGTH: 12241
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Pred. No. 2e-07;
0; Mismatches 184;
                                                                                                                                                                         NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
APPLICATION NUMBER: US/09/453,702B
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 57:
                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                          FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.5%;
Matches 188; Conservative (
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                                                                                                                                                      Sequence 2155, Application US/09134001C

Sequence 2155, Application US/09134001C

GENERAL INFORMATION:
GENERAL APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 2155
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Welch, Guy
Welch, Rod
Wildh, Rod
NUMBER OF SEQUENCES: 265
CORRESPONDE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 867;
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ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77.6; DB 4;
Pred. No. 9.4e-08;
0; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Mord Perfect 8.0 CURRENT APPLICATION DATA:
                                  360 TTTAGAATTAGAAACTATATCAAATA 386
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STREET: 1 South Pinckney Street
CITY: Madison
TTCAGAATTAGAAGAATACATTAAAAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGGTTTCATAAACTGAATCGAT 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2155
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US-09-453-702B-57/c
; Sequence 57, Application US/09453702B
; Patent No. 6365723
; Patent INFORMATION:
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Best Local Similarity 61.3<sup>5</sup>
Matches 125; Conservative
                                                                                                                      RESULT 2
US-09-134-001C-2155/c
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                                                                                                                                                                                     Length 447;
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                                                                                                                                                                             Query Match 7.2%; Score 68.6; DB 4; 1
Best Local Similarity 49.3%; Pred. No. 6.1e-06;
Matches 179; Conservative 0; Mismatches 184;
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TITLE OF INVENTION: REGULATION OF EXOPROTEIN IN
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COMPUTRY: United States
ZIP: 22313-1404
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: ISM PC compatible
COMPUTER: STATES: PC COMPATIBLE FORM:
COMPUTER: ISM PC compatible
COMPATING SYSTEM: PC-DOSS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,782
FILING DATE: 08-UUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,505
FILING DATE: 25-WAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFENCE/DOCKET NUMBER: 016921-092
TELECOMMINICATION: TELEPHONE: (703) 836-6620
                                  TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-676-782-10
Sequence 10, Application US/08676782
Patent No. 5976792
GENERAL INFORMATION:
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                                                                                                               US-09-134-001C-277
   LENGTH: 447
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Sequence 2777, Application US/09134001C
GENERAL INFORMATION:
GENERAL ING DATE:
GENE
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7.9%; Score 75.2; DB 4; Length 13737;
Best Local Similarity 86.5%; Pred. No. 4.6e-07;
Matches 83; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                          7.9%; Score 75.2; DB 4; Length 12241; 86.5%; Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-09-538-414-10
                                                                                                                                                                                                                        0; Mismatches 13; Indels
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APPLICANT: Salmeron, J.
APPLICANT: Salmeron, J.
APPLICANT: Salmeron, J.
APPLICANT: Rendra, D.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/O9/538,414
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 10
LENGTH: 13737
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATATCAATAAGTIGGAGTCAITACCGAATTTTTATA 96
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; TYPE: DNA
; ORGANISM: vector, multiple sequences
US-09-948-138-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09538414
Patent No. 6346655
GENERAL INFORMATION:
                                                                                                                                                                                                                        83; Conservative
                                                                                                                                                  Query Match
Best Local Similarity
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US-09-134-001C-2777
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                                                                                                                                                                                                                             7.1%; Score 67.2; DB 2; Length 1349; ilarity 49.2%; Pred. No. 1.4e-05; Conservative 0; Mismatches 183; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/248,505
FILING DATE: 24-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGRYT INFORMATION:

NAME: CLANE FEULY, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 016921-018
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Burns, Doane, Swecker & Mathis P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: CHEUNG, Ambrose
APPLICANT: CHEUNG, Ambrose
TITLE OF INVENTION: SEGULATION OF EXOPROTI
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUTNS, Doane, Swecker & Mathi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08248505
Patent No. 5587288
                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                       CUENCH: 1349 base pairs
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 177; Conserv
                                                                                        TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                               US-08-676-782-10
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US-08-248-505-1
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84 AAAAAGTTTAATTAAAAAGGAATTTTCAATTAGCTTTGAAGAATTCGCTGTATTGACATA 143
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                                                                                                                                                                                                                                                                                   Length 393;
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CITY: Alexandria STATE: Virgin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-676-782-6
; Sequence 6, Application US/08676782
; Patent No. 5976792
; GENERAL INFORMATION:
APPLICANT: CHEUNG. Ambrose
APPLICANT: CHEUNG. Ambrose
TITLE OF INVENTION: REGULATION OF EXOPROTEIN IN
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 18
; CORRESCED: ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   Score 66; DB 1; Le
Pred. No. 2.1e-05;
0; Mismatches 190;
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08-JUL-1996
N: 435
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,505
FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTRY: 'Inited States
ZIP: 22313-1404
COMPUTER READBLE FORM:
COMPUTER: REPORT disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.6%;
Matches 180; Conservative
                   LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virginia
United States
SEQUENCE CHARACTERISTICS:
LENGTH: 393 base paire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 TIGCGITIAA 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAACTATAA 393
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                                                                                                                                                                                CDS
19..390
                                                                                                                                                                          , NAME/KEY:
, LOCATION:
US-08-248-505-1
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15641 ААААААТААААСААААСБАБСААБААДААБААААСАТТААААААААА---АТАТАТАТС 15697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 AAATAAAAAAATATCAATAAGTTGGAGTCATTACCGAATTTTTATACTTATTGTTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 ATGAACTTTATAACATAGTTGGATAGAGTTTTCGATTTAATACATTAAATGTGAACCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 TGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTTAAGAAGTGAGTCTAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           471 AACAGITATIGITIAIGITACAGATACACAAAAAGCAAATATICAAAAACTGAITITCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 ATTAGAAGAATACATTAAAAATTAAATCAAGGTTAATTGCGTTTAATAACATTGAACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 AACAATTTATTAATACGAAGTTATTTTATTCAGCATTGGGACATAAAATTAACTTAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 CTACAACAAGAFGTGCATCAGAAGGAGTGGTTTAATAATGAGTAAAATTAATGATATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 AATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACTATTTAACTAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 19124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILNG DATE: US-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BTABLECANTON NUMBER: 29,655
REGISTRATION NUMBER: WH121.001CP1
TELEFANCE/DOCKET NUMBER: NH121.001CP1
TELEFANCE/DOCKET NUMBER: NH121.001CP1
TELEFANCE/DOCKET NUMBER: NH121.001CP1
TELEFANCE (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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Pred. No. 5.2e-05;
0; Mismatches 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.9%;
Best Local Similarity 46.3%;
Matches 296; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                         MEMOTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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US-08-487-826B-13
Sequence 13, Application US/08487826B
Sequence 13, Application US/08487826B
Setent No. 593327
GENERAL INFORMATION:
APPLICANT: Sim, Kim i.
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellams, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 AAAACGTAATGAGCATGATGAAGAACTGTATTAATTCTTGTTAATGCACAACAAGTAA 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 48.6%; Pred. No. 2.1e-05; Similarity 68.6%; Pred. No. 2.1e-05; S0; Conservative 0; Mismatches 190; Indels
                                      NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 016921-092
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-2021
TELEPHONE: (703) 836-2021
TELEPHONE: GRARACTERISTICS: LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.6'
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     19..393
                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                         ), NAME/KEY: CDS
; LOCATION: 19...
US-08-676-782-6
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1878 ATAATTAAAAAGAATTCTCAATCAGCTTTGAAGAATTTGCAGTATTAACTTATATTAGT 1819
                                               1698 AATGAACACGATGAAAGAACTGTTTTAATCTTAGTAGATTCTAAGCAGCGTAAAAAATC 1639
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454 AGTTTACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATT 513
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                                                                                                                                                                                                                                                          Sequence 6, Application US/08920827

Patent No. 5770375

GENERAL INFORMATION:

PAPPLICANT: Ohno, Tsuneya

APPLICANT: Matsuhisa, Akio

APPLICANT: Harousa, Akio

APPLICANT: Matsuhisa, Akio

APPLICANT: Harousa, Akio

APPLICANT: Harousa, Akio

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: Gloud Sears Tower, 233 South Wacker Drive

CITY: Chicago Sears Tower, 233 South Wacker Drive

CITY: United States of America

STREET: Hollois

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DetentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/920,827
                                                                                                                                               1638 GATGATTTACTTAAACGAGTAACAACCGTATCACAGAAGCAAATAATG 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                     514 CAAAAACTGATTTCAGAATTAGAAGAATACATTAAAAATTAAATCAAGG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 8654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64.2; DB 1; 1
Pred. No. 8e-05;
0; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus epidermidis
STRAIN: Clinical Isolate SE-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19036/32420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIDGE APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTOMERY AGENT INFORMATION:
NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/920,827
29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%;
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Best Local Similarity 49.0%
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: (ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                    US-08-920-827-6/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1878 ATAATTAAAAAAAATTCTCAATCAGCTTTGAAGAATTTGCAGTATTAACTTATATTAGT 1819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1758 CCTCAAGTTGTTAAAGCTGTTAAAATTTATCTCAAGAAATTACTTTAATAAAAAAGGT 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 GATACAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTTA 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACTATTTAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AAAATTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64.2, DB 1, Length 8654, Pred. No. 8e-05, 0, Mismatches 178; Indels 0
                                                                                                                                                                                                  APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                               E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
  15938 TAATTAAATAAAAAAAAAAAAAAAAAAAAATAAATTAATTACATGC 15976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Staphylococcus epidermidis
Clinical Isolate SE-22
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                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
                                                                                                                       Sequence 6, Application US/08920812
Patent No. 5763188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 49.0%;
Matches 171; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 8654 hard
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                                                                                                                                                                          GENERAL INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 s
CITY: Chicago
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MOLECULE TYPE: (
ORIGINAL SOURCE:
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                                                                          RESULT 11
US-08-920-812-6/c
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878 ATAATTAAAAAGAATTCTCAATCAGCTTTGAAGAATTTGCAGTATTAACTTATATTAGT 1819
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                                                                                                                                                                       394 TACTATTTAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAGA 453
274 GATACAAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTTA 333
                                                                                     334 AGAAGTGAGTCTAACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08362577C

Patent No. 5807673

GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Bda, Soji
TITLE OF INVENION:
Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        514 CAAAAACTGATTTCAGAATTAGAAGAATACATTAAAAATTAAATCAAGG
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CITY: Chicago
STATE: 1111noted States of America
CUTY: United States of America
ZIP: 60606-6402
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
FILING DATE: 27-MAR-1995
FILING DATE: 27-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 64.2; DB 1; ilarity 49.0%; Pred. No. 8e-05; Conservative 0; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Staphylococcus epidermidis
Clinical Isolate SE-22
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REGISTRATION NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 190
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic DNA
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 171; Conserv?
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STREET: 63
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                                                                                                                                                                            1758 CCTCAAGTTGTTAAAGCTGTTAAAATTTATCTCAAGAAATTACTTTAATAAAAAAGCGT 1699
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                                            394 TACTATTTAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAGA 453
                                                                                                                                 454 AGITTACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAATATT
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Pred. No. 8e-05;
0; Mismatches 178; Indels 0
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APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhara, Akio
APPLICANT: Wetsura, Akio
APPLICANT: Bda, Soji
ITILE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCE: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6310 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
CONTRY: United States of America
ZIP: 60606-642 FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Staphylococcus epidermidis
Clinical Isolate SE-22
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08921177 Patent No. 5798211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION: 312/474-6300
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Best Local Similarity 49.0%;
Matches 171; Conservative
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: Genomic DNA
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
ORIGINAL SOURCE:
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STATE: I.
COUNTRY:
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US-08-921-177-6
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1698 AATGAACGATGAAGAACTGTTTTAATCTTAGTAGATTCTAAGCAGCGTAAAAAATC 1639
.938 AAAATCAATGACTGCTTTGAATTATTAGCTATGGTCACTTATGCTGACAGATTAAAAAGGA 1879
                                                                                           1878 ATAATTAAAAAGAATTCTCAATCAGCTTTGAAGAATTTGCAGTATTAACTTATATTAGT 1819
                                                                                                                                                                                    1758 CCTCAAGTTGTTAAAGCTGTTAAAAATTTATCTCAAGAAATTACTTTAATAAAAAAGGT 1699
                                                 274 GATACAAAAAGGAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTA 333
                                                                                                                                             334 AGAAGTGAGTCTAACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCT 393
                                                                                                                                                                                                                                      394 TACTATTTAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAGA 453
                                                                                                                                                                                                                                                                                                                               AGTITACAAGACGAAAGAAGAGTIAITGITIAIGTIACAGATACACAAAAAGCAAATAIT 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Watsuhisa, Akio
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
CORRESPONDENCE 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920.828
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Clinical Isolate SE-22
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FILING DATE: 29-A0G-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-YAR-1995
ATTORNEY/AGENT INFORMATION:
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: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of Americ
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08920828
Patent No. 5853998
GENERAL INFORMATION:
APPLICANT: Onno, Tsuneya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REPERENCE/DOCKET UNMER: 1903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic DNA
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LENGTH: 8654 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
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STREET: 50...
TTV: Chicago
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US-08-920-828-6/c
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878 ATAATTAAAAAGAATTCTCAATCAGCTTTGAAGAATTTGCAGTATTAACTTATATTAGT 1819
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                                                                 Gaps
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      Length 8654;
Query Match
6.8%; Score 64.2; DB 2; Length 8
Best Local Similarity 49.0%; Pred. No. 8e-05;
Matches 171; Conservative 0; Mismatches 178; Indels
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Sequence 4, Appli Sequence 57, Appl Sequence 34, Appl Sequence 13, Appl Sequence 1190, Ap Sequence 128, Appl Sequence 128, Appl Sequence 128, Appl Sequence 253, Appl Sequence 233, Appl Sequence 233, Appl Sequence 231, Appl Sequence 25, Appl Sequence 27, Appl Sequence 28, Appl Sequence 128, Appl Sequence 182, Appl

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7 TILE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN TILE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN TILE OF INVENTION: COMPOSITION SELECTION NUMBER: US/10/043,539

7 TILE OF INVENTION: BACTERIA

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7 TILE OF INVENTION: BACTERIA

7 TILE OF INVENTION NUMBER: US/10/043,539

7 CURRENT FILING DATE: 2001-01-12

8 PRIOR PELING DATE: 2001-01-12

9 PRIOR PELING DATE: 2001-01-13

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ALIGNMENTS
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NAME/KEY: CDS
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
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15: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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14 US-10-14-170-57

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12 US-10-027-632-113786

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US-10-043-539-19
Sequence 19, Application US/10043539
Publication No. US20030114650A1
PUBLICANT: Cheung, Ambrose
APPLICANT: Manna, Adar
APPLICANT: Zhang, Gongyi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS:
TITLE OF INVENTION: CAPERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAAAACTGATTTCAGAATTAGAAGAATACATTAAAAATTAAATCAAGGTTAATTGCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 TACTATITAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAAATTGTTATCAAAGAAAAGA
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COUNTY.
Z19: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
MEDIUM TYPE: Medita 486/33
MADITER: HP Vectra 486/33
MADITER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           634 AAAATTAACTTAAAATTTAAATATGAAGA 663
                                                                          COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: EFILING DATE:
FILING DATE:
TELECOMMUNICATION NUMBER: BB248PP
REGISTRATION NUMBER: BB248PP
REJECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEFOND TO SEQ ID NO: 1525:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 Dase PAIRS
TELEFAX: number SEQ ID NO: 1525:
LENGTH: 400 Dase PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : LENGTH: 400 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: linear

US-08-781-986A-1525
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Matches 388;
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Sequence 1525, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 525
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 89410 Key West Avenue
CITY: Rockville

US-08-781-986A-1525

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1713770
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Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                              <u>AATAATGAGTAAAATTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAA</u>
                                                                                                                                                                             1713827 ATATATAAAATATATATATATATATAAATATAAAAT--ATATATAAAATATAAAA
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                                                                                                                                      GTTTTTCAGAGATACAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAA
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COPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/781,986A
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REGISTRATION NUMBER: 30,446
REPERENCE/DOCKET NUMBER: PB248PP
TRLECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1713414 AATATATATATATATAT 1713397
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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FILING DATE:
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US-08-781-986A-1599/c
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Publication No. US20030186277A1
GENERAL INFORMATION

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des PILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTTCAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGGCATTTTTTGAAAATAAAAA 60
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                                                                                                                                                                                                                                                                                                                              Query Match 22.2%; Score 210; DB 14; Length 210; Best Local Similarity 100.0%; Pred. No. 2e-26; Matches 210; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.7%; Score 82.4; DB 12; Length
48.2%; Pred. No. 0.0012;
Live 0; Mismatches 341; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          1 GTTTTCAAAATCGGTGGAGGTGCATGAAAAGTTATTGG
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          CURRENT APPLICATION NUMBER: US/10/043,539
CURRENT APPLICATION NUMBER: US 60/261,233
PRIOR FILING DATE: 2002-01-11
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PACENTIN VERSION 3.1
SEQ ID NO 19
LENGTH: 210
TYPE: DNA
CREANISM: Staphylococcus aureus
US-10-043-539-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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27; Conservative
FILE REFERENCE: DC-0199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3673778
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Best Local S
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Best Local Similarity 50.5
Matches 188; Conservative
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US-10-027-632-113786
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LENGTH: 3252
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Best Local Simi
Matches 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perna, Valerie
Penna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. US20030023075Alel Sequences of E. c
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: W1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ы
Ш
                                                                                                                                                        8.4%; Score 79.4; DB 8; Length 101; 92.2%; Pred. No. 0.00015; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                    156 TAAATGTGAACCTTGCTACAACAAGATGTGCATCAGAAGGAG 197
                                                                                                                                                                                                                                                                                                                            96 ACTTATTTGTTTAGAATGAACTTTATAACATAGTTGGATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01.Apr-2002
CLASSIFICATION: <a href="https://doi.org/10.10/114/">UNKNOWN></a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-114-170-57/c
Sequence 57, Application US/10114170
Feblication No. US20030023075A1
CENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Inner: MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: US-10-114-170-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
TELEFAX: (301) 309-8512 INPORMATION FOR SEQ 1D NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 101 base pairs
                                                    101 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                               Conservative
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                                                                                                          linear
                                                                                                                                                                           Best Local Similarity
Matches 94; Conserv
                                                                      ; TYPE: nucleic
; STRANDEDNESS:
; TOPOLOGY: lin
US-08-781-986A-1599
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                                                                                                                                                              Query Match
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Length 87563;

DB 14;

Score 77.6;

8.2%;

Query Match

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57122 ccercreacarerreadecearrecarrearrearrancecadergerragaaagraace 57063
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Sequence 113766, Application US/10027632

Publication No. US20030204075A9

GENERAL INCRMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION: POLYMorphisms in the Human Genome
FILE MEPERENCE: 108827.129

CURRENT PILNG DATE: 2002-04-30

FRIOR FILING DATE: 2000-07-12

FRIOR FILING DATE: 2000-07-12

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-00-28

FRIOR FILING DATE: 1999-00-28

FRIOR FILING DATE: 1999-00-28

FRIOR FILING DATE: 1999-00-38

FRIOR FILING DATE: 1999-00-38
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Mismatches 184; Indels
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Pred. No. 0.0013;
0; Mismatches 444;
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ORGANISM: Human

TYPE: DNA

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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-02-28
PRIOR PELICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFUMARE: FREESEQ for Windows Version 4.0
; LENGTH: 3252
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   TIGITIAGAAIGAACTITATAACATAGIIGGATAGAGIITITCGAITIAAIACATIAAAIG 161
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                                                                TGAACCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATAATGAGTAAAATTAA
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PILING DATE: 2000-03-29
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Publication No. US20030204075A9
GENERAL INFORMATION:
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       Length 3252;
                                                  Indels
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       DB 12;
     Score 76.6; DB 12;
Pred. No. 0.0013;
0; Mismatches 444;
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similarity 45.0%; Conservative 0
                         Local Simi
     Query Match
Best Local S
Matches 368
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FITLE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 1000-02-28
PRIOR PRIOR DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/16,363
PRIOR APPLICATION NUMBER: US 60/16,363
PRIOR APPLICATION NUMBER: US 60/16,363
PRIOR APPLICATION NUMBER: US 60/16,368
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE FEALSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                               42 ATTITITGAAAATAAAAATAICAAIAAGTIGGAGICAITACCGAAIIIITAIACTIAI
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582 INGAACGADAACAATITAITAATACGAAGITAITTAITCAGCAITGGGACATAAAATTAA
                                                                                                                    CTTAAAATTTTAAATATTGAAGATGCTTTAAATTAAAGTTAAAGACCAGCCATACCTTATTT
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Pred. No. 0.0013;
0; Mismatches 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-10-027-632-113786

Sequence 113786, Application US/10027632
GENERAL INFORMATION:
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US-10-027-632-113786
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                                                                                                                                    TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymcrphisms in the Human Genome
FITLE OF INVENTION: Polymcrphisms in the Human Genome
FITLE REFERENCE: 108827.129
CURRENT PELING DATE: 2002-04-30
FRIOR PELICATION NUMBER: US 60/198,006
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PAPLICATION NUMBER: US 60/193,483
FRIOR PELING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: US 60/165,218
FRIOR APPLICATION NUMBER: US 60/165,363
FRIOR PELING DATE: 12000-02-24
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-09-28
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
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                                                      Sequence 113788, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 45.0 Matches 368; Conservative
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US-10-027-632-113788
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                                              ATATTATAATGTATTATATAATTAAATTTAATATATAACTTATTCATATGTTACCATACA 2244
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  AAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTTTAAGAAGTGA 341
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US-1U-U27'-A27-115/77
Sequence 113797, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delyanophisms in the Human Genome
FILE REPERENCE: 108827, 129
CURRENT PAPLICATION NUMBER: US 60/218,006
FRICA APPLICATION NUMBER: US 60/218,006
FRICA APPLICATION NUMBER: US 60/198,676
FRICA FILING DATE: 2000-07-12
FRICA FILING DATE: 2000-07-12
FRICA FILING DATE: 2000-03-29
FRICA APPLICATION NUMBER: US 60/183,483
FRICA FILING DATE: 2000-03-29
FRICA APPLICATION NUMBER: US 60/185,218
FRICA FILING DATE: 1999-11-23
FRICA FILING DATE: 1999-11-23
FRICA APPLICATION NUMBER: US 60/167,363
FRICA FILING DATE: 1999-08-09
FRICA TILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                             AGACGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATTCAAAAACT
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; ORGANISM: Human
US-10-027-632-113787
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                                                                                                                                                                                                                                                                               2008 AACCAGATTAATAAGTTAATTTAATATTAATTAATT---TAATGTAAGTTAACAATAA 2064
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                                                                                                          42 ATTITIGAAAATAAAAAATAICAATAAGTIGGAGICATIACCGAAITITIAIACTIAI
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                                                      Gaps
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide;
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/27,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
                                                   5
   Length 3252
                                                   Indels
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                                                      0; Mismatches 444;
Score 76.6; DB 13;
Pred. No. 0.0013;
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8.1%;
ilarity 45.0%;
Conservative
   Query Match
Best Local Similarity
Matches 368; Conserv
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-10-027-632-113788
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US-09-912-020-468/c
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US-10-122-085A-5/c
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45.0%; Pred. No. 0.0013;
ive 0; Mismatches 444;
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PPLICATION NUMBER: US 60/193,483
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: -1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOCTWARE: FRASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.0
Matches 368; Conservative
                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113788
                                                                                                                                                                                                                                                                             SOFTWARE: FastSI
SEQ ID NO 113788
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APPLICANT: Greenlee, winner and Sullivan, P.C.
APPLICANT: Greenlee, winner and Sullivan, P.C.
APPLICANT: JOHN, Peter C.L.
APPLICANT: SEX, Francis J.
APPLICANT: SEX, Francis J.
APPLICANT: SEX, Francis J.
APPLICANT: SEX, Francis J.
APPLICANT: VAN CAMP, Wim J.
TITLE OF INVENTION: METHOD OF MODIFYING PLANT CHARACTERS BY THE TARGETED EXPRESSION OF TITLE OF INVENTION: GYCLE CONTROL PROTEIN
FILE REFERENCE: DOCKET 19-00A
CURRENT APPLICATION NUMBER: US/10/122,085A
CURRENT APPLICATION NUMBER: US 09/513,504
PRIOR FILING DATE: 2000-02-25
                                                                                2185 ATATTATAATGTATTATAATTAAATTTTAATATATTAACTTATTCATATGTTACCATACA 2244
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762 ATCAAGTTTACGATCATAAATATTTTCTGCGATATAGCTTTGGATGGTTCCAAGTATTTT 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Foreyth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
APPLICANT: Tramico, Robert T.
APPLICANT: Yanamorto, Robert T.
APPLICANT: Yanamorto, Robert T.
APPLICANT: Yanamorto, Robert T.
APPLICANT: W. H. Howard
TITLE OF INVENTION: EGENERICHIA COLI
FILE REFRENCE: ELITRA.0010V1
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT FILING DATE: 2001-07-23
PRIOR FILING DATE: 2001-01-27
PRIOR FILING DATE: 1999-01-27
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Pred. No. 0.0011;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                                      2245 CAGTTAAATATATATACAGTATAAACATATTAAACT 2281
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 468, Application US/09912020
Patent No. US20020045592A1
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10122085A Publication No. US20030172404A1 GENERAL INFORMATION:
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Best Local Similarity 76.2%;
Matches 93; Conservative
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, ORGANISM: Escherichia coli
US-09-912-020-468
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PRIOR APPLICATION NUMBER: US 60/121,870

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RESULT 15

105-10-033-190-5

105-10-033-190-5

105-10-033-190-5

105-10-033-190-5

105-10-033-190-5

105-10-033-190-5

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105-10-033-190-6

105-10-033-190-7

105-10-033-190-7

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7.9%; Score 75.2; DB 13; Length 12241;
Best Local Similarity 86.5%; Pred. No. 0.0034;
Matches 83; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                        Query Match
Pest Local Similarity 86.5%; Pred. No. 0.0033;
Matches 83; Conservative 0; Mismatches 13; Indels 0;
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Job time : 374 secs
                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Cloning vector pBin19 US-10-122-085A-5
PRIOR FILING DATE: 1999-02-26
PRIOR PEDLICATION NUMBER: US 60/149,049
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 11777
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial
FEATURE:
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CNSOOEVL 101 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL069706
AL069706
GSS.
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Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
Web: www.genoscope.ons.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Droscopial Genome Project (BDGP).
The BDGP is constructing a physical map of the Droscophila melanogaster genome using these BACs. For further information please see http://www.fruiffly.org The BDGP Droscophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Brosophila.
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BX458623
CNSO4D07
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BX415878 BX415878
BX415058 BX415058
                                                                                                                                   ; Search time 2414 Seconds
(without alignments)
9534.523 Million cell updates/sec
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, on bw sp, the same strain used for the BDGP from the and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                          /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BARR2923"
/clone lib="RRC1-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                     Similarity 36.1%; Pred. No. 4.2e-06; 29; Conservative 117; Mismatches 288;
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/tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMYSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized." 170 others
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                                                                                                                                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Library Enail: filang@lifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPOOSBE02QP1.
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                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1200)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/db_xref="taxon:9606"
/clone="CSOCAP008Y104"
GI:30765550
                                                          Homo sapiens (human)
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275; Conserv
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BX415878 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YI04 5-PRIME, mRNA sequence.

RESULT: 2 BX415878 LOCUS DEFINITION 938 328 388

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3-PRIME, MRNA sequence.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
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Faraday Avenue Genoscope sequence ID : CSOCAPO04AD10NP1.
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Catarrhini; Hominidae; Homo.
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1057 AWWAAAAWTWTAAWAAAAATTTTTTTTTTTAWAWWAAATAWAWTTTTAWAWWTWWATWW
                                                                                                             TCAGAGATACAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTAATATTTAAATCATA
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                                                                     TGAGTAAAATTAATGATATAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTT
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Mammalia, Eutheria, Primates,
1 (bases 1 to 1056)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cyoCAPD08X104"
/tissue_type="THYMUS"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Control National de Sequencage

BP 191 91006 EVRY codex - France

BP 191 91006 EVRY codex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

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                                                                     AGGITAATTGCGTTTAATAACATTGAACGATAACAATTTATTAATACGAAGTTATTATT
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Homo sapiens
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/tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pCW/VSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
175 others
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Drosophila melanogaster genome survey sequence TET3 end of BAC #BACRO8K10 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

LOCUS DEFINITION

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by 19 1000 by 19 2000 cours. Franch (E-Mail : SeqreteggHOSCODE-CHBILL - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila genome Project (BDCP). The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see thtp://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazucoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDCP from the isogenic strain y2; cn bw sp, the same strain used for the BDCP's Pl and EST library is nore detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
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Mismatches 265; Indels
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| Mol. type="genomic DNA"
| db xref="taxon:7227"
| clone="bACR08K10"
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BX43739 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008XG24
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Catarrhini, Hominidae, Homo.
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ACCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATAATAAGGAGTTAATGA
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cgi-bin/cluster.cgi?seq=CSODE014CC03NP1&cluster=3370.r. Contact
feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE014CC03NP1.
Location/Qualifiers
                                                                                                                 TTATTCAGCATTGGGACATAAAATTAAACTTAAAATTTAAATATTGAAGATGCTTTAATTA
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3370.r Imore information about this cluster, see
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library was not normalized."
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//clone_Tip="Homo sapiens THYMUS"
//note="Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EoRV sites of the pCMVSPORT 6 vector.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1045)

BX456814 1045 bp mRNA linear EST 22-MAY-2003 4-8456814 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP004Y019 3-PRIME, mRNA sequence. BX456814

BX456814.1 GI:31034806

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

Homo sapiens (human)

Homo sapiens

ORGANISM

REFERENCE

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BX462207.1 GI:31023422
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/mol type="mRNA"
/db_xref="taxon:9606"
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/clone Tib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; large strand cDNA was primed
/note="Vector: pcMVSPORT 6; large strand cDNA was primed
/with a NotI-oligo(dT) primer. Five prime end enriched,
/double-strand cDNA was digested with Not I and cloned
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized.

15 a 30 c 71 g 310 t 274 others
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Homo sapiens cDNA clone CS0CAP008YB01
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length, CDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 1 1006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com Uhttp://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO08CAOLQPI.
Location/Qualifiers
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                                                              903 GGATGTATTGCTATAAGAACTAATGGTTTCATAAACTGAA
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llarity 30.4%; Pred. No. 0.001;
Conservative 170; Mismatches 365;
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BX437758 HOMO SADIENS THYMUS
5-PRIME, MRNA SEQUENCE.
BX437758.1 GI:30773605
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/tissue type="B CELLS (RAMOS CELL LINE)"
/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; let strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
BE 106 EVRY cedex - France
Inbrary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 24.r For mo
information about this cluster, see http://www.genoscope.cns.fr/
ogi-bin/cluster.cgi?seq-CSODG004CA02QP1&cluster=24.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODG004CA02QP1.
                                                                                                                                                                             TTAWAWWTATRARGADTTTTTTATAWWTATTTTTTWWAWAAGATDKAAAAWWWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646 AAAITIAAATATIGAAGATGCTITAATTAAAGTTAAAGACCAGCCATACCTTATITCAGC
                                                           564 ITTITWWIWAWAAAASAGAWKAIWITITKKITIAIWWKRAGGAIWITITITIWIWAAR
                                                                                                                                                                                                                                                                         466 GAAAGAACAGTTATTGTTATGTTACAGATACACAAAAAGCAAATATTCAAAAAACTGATT
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346 AACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACTATTAACT
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/clone="CS0DG004YB03"
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**PCMVSPORT** 

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AAAAAAAAAAAAAAAAAAAAAATTTWTWAAAATAATYYCMCAAACAAAACCTACCC 1028
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1. (bases 1 to 1201)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
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                                                              Length 1201;
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BX420717 Homo sapiens FETAL BRAIN Homo sapiens CDNA (CSODF033YC10 5-PRIME, MRNA sequence.
                                                              ; Score 93.8; DB 13;
; Pred. No. 0.0025;
48; Mismatches 341;
the Not I and EcoRV sites of
Library was not normalized."
141 c 153 g 522 t
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BX420717.1 GI:30658996
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Homo sapiens
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/mol_type="mRNA"

/db_xref="Laxon:9606"

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/clone_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCWVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-srrand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

85 a 115 c 108 g 299 t 94 others
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF033BB05QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAAAGAAGTTTACAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.8%; Score 93.2; DB 13;
Best Local Similarity 42.4%; Pred. No. 0.003;
Matches 271; Conservative 52; Mismatches 311;
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RESULT 12 AL536104/c

Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France

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Query Match
Best Local Simi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_cype="FETAL BRAIN"
/dev_stage="fetal"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="forgan: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
119 c 146 g 409 t 168 others
                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1201)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12799597.
                                                                                                                                                                                                                                                                                                                                                                       URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           990 WITITIAMAIAMATWITUMIAWWWIAITIAAYWCWIAWIAIAIAITWIWWIWWIAWCIAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 CAAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGAGTCTAACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930 WATTWWWAWAATWWTWTAWAAWTTATAAATAAAAWATAAAWTTAAAATTAAAAWAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458 TACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATT-CAA
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                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
BP 191 91.006 EVRY cedex - France
Email: sequencecope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF022BB09QP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 92.8; DB 9; 35.1%; Pred. No. 0.0034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="CS0DF022YC18"
                                                                            AL536104.2 GI:31260974
                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                               Contact: Genoscope
                                                                                                                                    Homo sapiens
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Best Local Similarity
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ORIGIN
                     DEFINITION
                                                                                                                                  ORGANISM
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Gossypium arboreum
Gossypium arboreum
Gossypium arboreum
Gossypium arboreum
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bokaryota; Magnoliophyta; eudicotyledons; core eudicots; rosids;
curosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
I (Bases II to 887)
Mulny, R. A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
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fiber library Gossypium
                      631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gossypium arboreum"
/organism="ARA"
/strain='ARA"
/cultivar='8460"
/db xref='taxon:29729"
/clone='GA_Eb0021G05f"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rerahahahahahanninniharahaherahinninninahahahahanahahan
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/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
71 c 37 g 321 t 29 others
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Gaps
                                                                   697 TATTICAGCITATIAAGCITGACACAAGGIACACIAGICTITITATITITAATATITICIT
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                                                                                                                                                                                                                                                                                                                    887 bp mRNA linear GA Bb0021G05f Gossypium arboreum 7-10 dpa fiber larboreum cDNA clone GA Eb0021G05f, mRNA sequence. BF274559
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Pred. No. 0.0044;
0; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Uradan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High-quality sequence start: 2
High quality sequence stop: 881.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. coli"
                                                                                                                                                                   777
                                                                                                                                                                                                                550
                                                                                                                                                                                                                570 TGGAAAACAGTTTAATGATCA
                                                                                                                                                                     757 AGAAAATCAAGTTTACGATCA
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Homo sapiens
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Office of Cancer Genomics
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAO7 Bethesda, MD 20892
Email: cgapbs r@mail.inh.gov
Tissue Procurement:

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LibMid964g row: o column: 14
High quality sequence start: 49
High quality sequence store: 150.
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(bases 1 to 1123)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
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81 AGAGTICAAACCITACTATITAACTAAAGCITTACAAAAGCTAAAAAGATITAAAATIGIT
                                                                 441 ATCAAAGAAAAGAAGTITACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACA
                                                                                                AGCATTGGGACATAAAATTAAACTTAAAATTTTAAATATTGAAGATGCTTTAAATTAAAGTTA
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Xenopus laevis
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656 AITGAAGAIGCIIIAAITAAAGIIAAAGACCAGCCAIACCIIAITTCAGCIIAIIAAGCI 715
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/ organism="Mono sapiens"
/ mol_type="mRNA"
/ db xref="taxon:9606"
/ clone="CSOCAP008YB01"
/ tissue type="THYMUS"
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626 WHCYTTWAWAAAAAAAWAICCTYWWWATAAWWAAAWAAWATWWTCTSTTTTWTWAWWAA 567
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                                                                                                                                                                                Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedax - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Sequence In : CSOCAPOO8CAO1QP1.

Faraday Avenue Genoscope sequence ID : CSOCAPOO8CAO1QP1.
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                Mammalia; Eutheria; Primates; Catarrhin; Hor 1 (bases 1 to 1200)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Staphylococcus epi S. aureus regulato

Staphylococcus

S. aureus regularo l'actococcus lactis Staphylococcus aur Listeria monocytog Staphylococcus epi Listeria monocytog Plasmodium falcipa Rat syntaxin 5 pro Staphylococcus epi Human protein SEQ Human claspoolum falcipa Sequence of the Plasmodium falcipa Sequence of the Plasmodium falcipa Sequence of the Plasmodium falcipa Sequence Staphylococcus epi S. pneumoniae resp S. pneumoniae resp S. pneumoniae resp S. pneumoniae resp S. pneumoniae cep Human bone marrow Staphylococcus epi XisA recombinase pi NISA recombinase pi S. epidermidis ope Staphylococcus epi

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open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding a Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4993
                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                     AAO16359
ABG20278
AAB18280
AAB18280
ABB78326
AAW95087
AAW95087
AAW95087
                    ABP54930
ABB55470
ABB48360
ABB48360
AAB49262
AAB18273
AAM43423
AAM43045
AAM79481
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ABP40764
ABJ10468
ABJ10470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP40148 standard; Protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermidis;
gene therapy.
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WPI; 2002-381255/41.
N-PSDB; ABN92693.
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Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1998;
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08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-2002.
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372.522 Million cell updates/sec
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1 MSKINDINDLVNATFQVKKF.....DTQKANIQKLISELBEYIKN
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             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                           hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AAW14000
AAX50721
AAX50725
AAB68760
AAB68761
AAB68761
ABP40769
                                                       protein search, using sw model
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length: 2000000000
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                        Copyright
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Gapop 10.0
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Candida albicans

interfere with the expression of the toxins, thereby functioning as antimicrobial agents to render the microorganism avirulent. The DNA encoding this sequence can be used for diagnostic identification of pathogenic staphylococci which express the protein, and the resulting virulence factor.

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Gaps

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Indels

52;

; Score 148; DB 18; ; Pred. No. 5.6e-07; 27; Mismatches 52;

25.8%; 30.1%;

34; Conservative

Matches

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Local Similarity

Query Match

124 AA;

Sequence

88888888

Length 124;

9 62

1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 

61 KPYYLTKALOKLKULKLLSKKRSLQDERTVIVYVTDTOKANIQKLISELEEYI 113

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polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                            24-MAY-1994;
                                                                                                                                 24-MAY-1994;
                                                96;
                                                                                                                   JS5587288-A
                                                                                                                        24-DEC-1996
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                                                               61
                                       Sequence
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                                                    ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABPS-124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the staphylococcal accessory regulatory (SAR) A protein of Staphylococcus aureus. The SAR protein controls the pryression of potential virulence factors, such as bacterial endotoxins. The SAR locus is thought to regulate exoprotein genes positively, at the mRNA level. This protein can be used for designing analogues which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGKIKDINDLVNATFQVKKFFRDTKKQYNLNYEEIYILNHILKSESNEISSKEIATCSEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         occal accessory regulatory A protein, sar, virulence factor, endotoxin, regulatory protein, exoprotein gene; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPYYLTKALOKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated staphylococcal accessory regulatory protein and gene used to develop prods. for use as antimicrobial agents and for detection of pathogenic staphylococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 486; DB 23;
Pred. No. 3.2e-40;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcal accessory regulatory A protein.
Disclosure; SEQ ID 4993; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 9-10; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW14000 standard; Protein; 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial endotoxin;
antimicrobial agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-064792/06.
N-PSDB; AAT60281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    USPTO web site.
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accessory regulatory procein (TI), designated sar) which regulates the expression of S. aureus exoprotein virulence determinants (EVD). (I) controls the expression of virulence determinants such as endotoxins in S. aureus. (I) is used to design analogs that interfere with expression of EVD, i.e. potential antibacterial agents and for generating specific antibodies which are used to detect (I) in microbial isolates or for affinity purification of (I). The nucleic acid (II) that encodes (I) or its fragments) can be used to identify S. aureus that express sar (and thus EVD) by usual hybridization and amplification tests, also for recombinant production of (I). This sequence represents the Staphylococcus aureus sarA protein which is described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w accessory regulatory protein, sar, from Staphylococcus aureus, used design analogs potentially useful as antibacterial agents -
                                                                                                                                                                                                                                         Staphylococcal accessory regulatory protein; sar protein; endotoxin; exoprotein virulence determinant; EVD; antibacterial agent; detection.
63 KQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel full-length Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 25-28; 30pp; English
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                                                                                                  AAY50721 standard; Protein; 124
                                                                                                                                                                                                                                                                                                                                                                                                    96US-0676782
                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0248505
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheung A, Fischetti VA;
                                                                                                                                                                                                         S. aureus sarA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SIGA-) SIGA PHARM INC.
                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-021938/02.
N-PSDB; AAZ24204.
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                                                                                                                                                                      08-FEB-2000
                                                                                                                                                                                                                                                                                                                               US5976792-A.
                                                                                                                                                                                                                                                                                                                                                                02-NOV-1999
                                                                                                                                    AAY50721;
                                                               RESULT 3
                                                                                    AAY5072
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DB 21; Length 124;

25.8%; Score 148;

Query Match

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The present sequence is given in a specification relating to a method for identifying inhibitors of SarA (staphylococcal accessory regulator) function involved in the expression of Staphylococcal virulence genes. The method comprises contacting a candidate inhibitor with a SarA binding site of the agr (accessory gene regulator) locus in solution and assessing the binding of the candidate inhibitor to the SarA binding site of the agr locus. The identified inhibitors are useful for preventing and treating staphylococcal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcal accessory regulatory protein; sar protein; endotoxin;
                                                                                                                                                                                                                                    Staphylococcus aureus; SarA; staphylococcal accessory regulator A; agr; accessory gene regulator; antibacterial; SarA inhibitor; virulence gene; staphylococcal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying inhibitors of staphylococcal SarA (accessory regulato) which are useful for treating staphylococcal infections, comprises using specific binding sites of SarA protein on an accessory gene regulator locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.8%; Score 148; DB 22;
ilarity 30.1%; Pred. No. 5.6e-07;
Conservative 27; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rechtin TM;

    epidermidis sarA protein fragment.

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                                                                 Ä.
                                                                                                                                                                                                 Staphylococcus aureus SarA protein.
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                                                               AAB68760 standard; protein; 124
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                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
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Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             WO200103686-A2.
                                                                                                                                                                                                                                         Staphylococcus agr; accessory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hurlburt BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1999;
                                                                                                                                                      17-APR-2001
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                                                                 1 MSKINDINDLVMATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKBIAKCSEF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcal accessory regulatory protein; sar protein; endotoxin; exoprotein virulence determinant; EVD; antibacterial agent; detection.
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                       52; Indels
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5.6e-07;
                       Mismatches
30.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Column 31-32; 30pp; English.
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                       27;
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Best Local Similarity
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9 62 (GENO-) GENOME THERAPEUTICS CORP.

Bush D;

Doucette-Stamm LA,

WPI; 2002-381255/41.

97US-064964P.

08-NOV-1997;

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This invention describes a novel full-length Staphylococcus aureus accessory regulatory protein ([1], designated sar) which regulates the expression of S. aureus exoprotein virulence determinants (EVD). (I) controls the expression of virulence determinants such as endotoxins in S. aureus. (I) is used to design analogs that interfere with expression of EVD, i.e. potential antibacterial agents and for generating specific antibodies which are used to detect (I) in microbial isolates or for affinity purification of (I). The nucleic acid (II) that encodes (I) or its fragments) can be used to identify S. aureus that express sar (and thus EVD) by usual hybridization and amplification tests, also for recombinant production of (I). This sequence represents a Staphylococcus aureus sarA protein which is described in the method of the invention.
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                                                                                                                                                                                                                                                                            New accessory regulatory protein, sar, from Staphylococcus aureus, used to design analogs potentially useful as antibacterial agents -
 exoprotein virulence determinant; EVD; antibacterial agent; detection.
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                             Staphylococcus epidermidis.
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Best Local Simi
Matches 33;
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 KIDSIFNTIKKKYGMSKBEILILLLTLL--EKGSMTLKEMDKYVHIKPYKRTRTYNNLVNL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis; SarA; staphylococcal accessory regulator A; agr; accessory gene regulator; antibacterial; SarA inhibitor; virulence gene; staphylococcal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 QVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDL
                                                                                                                                               Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 149;
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                                                                                                                                                                                                 Disclosure, SEQ ID 5151; 267pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 149 AA;
                                                                                                                N-PSDB; ABN92851
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Matches 23; Conserv
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                                                      The present sequence is given in a specification relating to a method for identifying inhibitors of SarA (staphylococcal accessory regulator) function involved in the expression of Staphylococcal virulence genes. The method comprises contacting a candidate inhibitor with a SarA binding site of the agr (accessory gene regulator) locus in solution and assessing the binding of the candidate inhibitor to the SarA binding site of the agr locus. The identified inhibitors are useful for preventing and treating staphylococcal infections.
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specific binding sites of SarA protein on an accessory gene
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                                   Disclosure, Page 13; 79pp; English.
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Best Local Similarity 29.2<sup>3</sup>
Matches 33, Conservative
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08-NOV-1997;
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 249;
                                                                                                                                                                                            Length 148;
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28.8%; Pred. No. 0.078;
iive 20; Mismatches 36;
                                                                                                                                                                                        24.9%; Score 143; DB 23; 29.2%; Pred. No. 2.2e-06; ive 25; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP40173 standard; Protein; 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-055779P.
97US-064964P.
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                                                                                                                                                                                                                          Local Similarity 29.2 tes 33; Conservative
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ABP54930 standard; Protein; 134 AA.
 ABP54930
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               Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleid caid sequences which encode the amino acid sequences given in ABB35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can for compounds able to interfere with the S. epidermidis life screen for compounds able to interfere with the S. epidermidis life N. B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
IYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVTV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 VTELALDTGTVSPLLKRAEQVDLIKRERSEVDQREVFIHLTDKSEM-IRPELSNASEKV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKINDIND-----LVNATFQVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 MSEQHNLKEQLCFSLYNAQRQVNRYYSNKYFKKYNLTYPQFLVLT-ILWDES-PVNVKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                       Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5581.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.5%; Score 94.5; DB 23; Length 154; 25.2%; Pred. No. 0.13; ive 34; Mismatches 46; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID 5581; 267pp; English.
                                                                                                                       ABP40736 standard; Protein; 154 AA.
                                                         104 TONOCSKITOLIDELEHFLE 123
                                            TDTQKANIQKLISELEEYIK 114
                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                              98US-0134001.
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                                                                                                                                                                                                                                                                                                                                   97US-055779P
                                                                                                                                                                                                                        antibacterial; gene therapy
                                                                                                                                                                                                                                            Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                       Bush D;
                                                                                                                                                                  24-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABN93281
                                                                                                                                                                                                                                                                                                              13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                   14-AUG-1997;
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                                                                                                                                             ABP40736;
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a mutant RAT (regulatory of autolytic activity) protein of Staphylococcus aureus. It is encoded by a mutant RAT gene (see ABV7308) identified in a Th551 transposon library of S. aureus strain RN6300. Transposon insertion results in a truncated RAT coding sequence, yielding a protein missing the last C-terminal 13 amino acids of the wild-type protein sequence (see ABP5429). A RAT mutant strain displayed significantly enhanced autolytic activity as compared with the parent. In the presence of penicillin, the RAT mutant showed increased lysis as compared with wild-type S. aureus. The invention provides RAT gene and RAT mutant mucleic acid sequences, the polypeptides encoded by these genes, vectors and sequences, the polypeptides encoded by these genes, or the polypeptides encoded by the autolytic activity of S. aureus and other bacteria through interaction with the RAT gene, RAT mutant gene, or the polypeptides condition of growth of S. aureus and other bacteria and in the tranship of growth of S. aureus and other bacteria and in the tranship with an antibiotic such as penicillin to promote lysis of the bacterial. The RAT gene and gene products are also useful as research tools to enhance the understanding of the autolytic research tools to enhance the understanding of the autolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New regulator of autolytic activity (RAT) nucleic acid sequences and polypeptides, useful for regulating the autolytic activity of bacteria, inhibiting bacterial growth and infectivity, or for treating bacterial
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                                                                                                                                                                                                            Regulator of autolytic activity; RAT; autolysis; antimicrobial; antibacterial; screening; mutant; mutein.
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    S. aureus regulator of autolytic activity (RAT) mutant protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOKLKDLKLLSKKRSLQDERTVIVYVTD 96
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15-AUG-2001; 2001US-312546P.
12-OCT-2001; 2001US-329140P.
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Best Local Similarity 28.4%
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
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                                                                    08-JAN-2003
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ABP54930;
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The present sequence is a novel regulatory of autolytic activity (RAT) protein of Staphylococcus aureus, which is involved in the control, modulation or regulation of autolytic activity. This 17 kDa protein (predicted pI 7.38) is encoded by a novel gene (see ABUY3907) that was identified in a Th51 transposon library of S. cureus strain RN6390 by screening for genes that affected expression of genes encoding the capsular polysaccharide of S. aureus. The invention provides RAT gene and RAT mutant nucleic acid sequences, the polypeptides encoded by these genes, vectors and host cells, and a method of identifying agents that modulate the aucolytic activity of S. aureus and other bacteria through interaction with the RAT gene, RAT mutant gene, or the polypeptides encoded by them. These agents are expected to be useful in the inhibition of growth of S. aureus and other bacteria and in the treatment of bacterial infection. The RAT gene or gene products are also useful as research tools to enhance the understanding of the autolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LVNATFQVKKFFRD-TKKKFNLNYEBIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New regulator of autolytic activity (RAT) nucleic acid sequences and polypeptides, useful for regulating the autolytic activity of bacteria, inhibiting bacterial growth and infectivity, or for treating bacterial
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                                       Staphylococcus aureus regulator of autolytic activity (RAT).
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16.3%; Score 93.5; DB 23;
Best Local Similarity 28.4%; Pred. No. 0.16;
Matches 25; Conservative 25; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                               15-AUG-2001; 2001US-312546P.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                             (DART-) DARTMOUTH COLLEGE
                                                                                                    antibacterial; screening
                                                                                                                                            Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-750455/81.
N-PSDB; ABV73907.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 AA;
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08-JAN-2003
                                                                                                                                                                                                                             12-SEP-2002
                                                                                   Regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention is related to a Lactococcus lactis nucleotide sequence (ABA9051) and related proteins (ABB53300-ABB55621). The nucleic acid sequence; suseful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-07-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSLANQIDQFLGTIMQ----FAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                    Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlich SD;
  LKRMEQVDLIKRERSEVDQREVFIHLTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; SEQ ID No 2172; 2504pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INRG ) INRA INST NAT RECH AGRONOMIQUE
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                                                                                                    ABB55470 standard; Protein; 144 AA
                                                                                                                                                                                                                               Lactococcus lactis protein zitR
                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                            Lactococcus lactis IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
----- 34; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-043418/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 AA;
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                                                                                                                                                                                     16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolotine A,
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  73
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ABP54929 ID ABP5 XX AC ABP5 XX

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Antibacterial; gene therapy, vaccine, biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
    Listeria monocytogenes protein #1064.
                                                11-APR-2001; 2001WO-FR01118.
                                                        11-APR-2000; 2000FR-0004629.
                        Listeria monocytogenes
                               WO200177335-A2
                                        18-OCT-2001
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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and to his synthesis and blodegradation, especially blosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes. Talated diseases. In addition, the genome sequence and proteins encoded by it are addition, the genome compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.

Note: The sequence dated for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.

The province of the printed by the printed specification, but was obtained in electronic format directly from WIPO.

The province of the printed by the printed specification, but was obtained in electronic format directly from WIPO. Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Varquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charlit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Liopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides Claim 6; SEQ ID No 1065; 192pp; French. (INSP ) INST PASTEUR WPI; 2002-010914/01. 141 AA; Voss H; Seguence Rose M,

ď 7 INDLVNATFQVKKFFRDTK-KKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYL 65 5; Gaps Query Match 16.1%; Score 92.5; DB 23; Length 141; Best Local Similarity 23.6%; Pred. No. 0.19; Matches 25; Conservative 30; Mismatches 46; Indels 5 ò

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66 TKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEE 111

completed: November 17, 2003, 12:43:13 Search co Job time

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Best Local Similarity 84.2
Matches 96; Conservative
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Sequence 12, Appl
Sequence 13, Appl
Sequence 5151, Ap
Sequence 5614, Ap
Sequence 5018, Ap
Sequence 8073, Ap
Sequence 4980, Ap
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26170, A
3394, Ap
4, Appli
4421, Ap
4421, Appli
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2, Appli
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                                                                                                                                                          November 17, 2003, 12:42:30 ; Search time 21 Seconds (without alignments) 231.702 Million cell updates/sec
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574
1 MSKINDINDLVNATFQVKKF.....DTQKANIQKLISELEEYIKN
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1. /GGTZ 6/prodata/2/iaa/5A_COMB.pep:*

2. /GGTZ 6/prodata/2/iaa/5B_COMB.pep:*

3. /GGTZ 6/prodata/2/iaa/6A_COMB.pep:*

4. /GGTZ 6/prodata/2/iaa/6B_COMB.pep:*

5. /GGTZ 6/prodata/2/iaa/PCTUS COMB.pep:*

5. /GGTZ 6/prodata/2/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-676-782-12

US-09-134-001C-5151

US-09-134-001C-51181

US-09-134-001C-5614

US-09-134-001C-5614

US-09-134-001C-5618

US-09-134-001C-4980

US-09-134-001C-4980

US-09-134-001C-4980

US-09-134-001C-4421

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US-09-139-064-2

US-09-139-064-2
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US-09-107-532A-7156
US-08-195-705-2
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US-09-572-191-2
US-09-723-262-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             - protein search, using sw model
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seq length: 2000000000
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Match Length
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Perfect score:
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Maximum DB
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No.
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Sequence 4993, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION WUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
NUMBER OF SEQ ID NOS: 5674
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4, Appli
10, Appli
4, Appli
5, Appli
           6512, Ap
5409, Ap
6403, Ap
8, Appli
5259, Ap
28, Appl
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4123, Ap
7414, Ap
8, Appli
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         US-09-107-532A-6512
US-09-107-532A-6512
US-09-107-532A-6403
US-08-107-532A-6403
US-08-107-532A-6403
US-08-108-60-64A-28
US-08-405-496A-28
US-08-415-136-28
US-08-415-434-4
US-08-458-819-4
US-08-458-819-4
US-08-458-819-4
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Sequence 12, Application US/08676782
Sequence 12, Application US/08676782
Sequence 12, Application US/08676782
Sequence 12, Application
Sequence 12, Application
APPLICANT: CHEUNG, Ambrose
APPLICANT: CHEUNG, Ambrose
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 18
CORRESSONDENCE ADDRESS:
ADDRESSED: BURNS, DOANE, SWECKER & MATHIS, L.L.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                           PCT US91.07035-4
US-09-508-370A-5
US-09-107-532A-6348
US-09-134-001C-4123
US-09-328-352-7414
US-09-322-184-8
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84.2%; Pred. No. 5.9e-44;
live 8; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4993
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Sequence 5614, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-0.07
CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5151, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               51; Indels
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; Pred. No. 3e-08;
27; Mismatches 51
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CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5151
LENGTH: 149
                                                016921-092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis
                            39,300
                    REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                         TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                               25.4%;
29.7%;
McGowan, Malcolm K
                                                                                                                                                                                             : 113 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               33; Conservative
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                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-676-782-13
                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-134-001C-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Staph
US-09-134-001C-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-134-001C-5614
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                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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25.8%; Score 148; DB 2; Length 124;
Best Local Similarity 30.1%; Pred. No. 2.1e-08;
Matches 34; Conservative 27; Mismatches 52; Indels
                                                                                                                                     CURRAINS SISIEM:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,782
FILING DATE: 08-ULL-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,505
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: MGGOWAN, MAICOIM K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 016921-092
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: CHEUNG, Ambrose
APPLICANT: FISCHETH, Vincent A.
TITLE OF INVENTION: REQULATION OF EXOPROTEIN IN
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: US/08/676,782
FILING DATE: 08-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,505
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08676782
Patent No. 5976792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 amino acids
  United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 08
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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US-08-676-782-13
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     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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18-09-134-001C-4980
Sequence 4980, Application US/09134001C
Sequence 4980, Application US/09134001C
Batch in C. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BEDERHIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US 60/9/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-10-08
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-10-08-14
SEQ ID NOS: 5674
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8073, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTG99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 150
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                                                                                                                                                                                                                                                                                                                                                                                                                        55 AKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
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                                                                                                                                                                                                                                                                                                                          1 MSKINDIND-----LVNATFQVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEI
                                                                                                                                                                                                                                                                                                                                                                     8 MSEQHNIKEQLCFSLYNAQRQVNRYYSNKVFKKYNLTYPQFLVLT-ILWDES-PVNVKKV
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15.8%; Score 90.5; DB 4;
Best Local Similarity 27.1%; Pred. No. 0.03;
Matches 26; Conservative 25; Mismatches 42;
                                                                                                                                                                                                                              16.5%; Score 94.5; DB 4;
25.2%; Pred. No. 0.012;
                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.2%; Pred. No. 0.012
Matches 30; Conservative 34; Mismatches
       PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5581
LENGTH: 154
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                                                                                                                                                      ORGANISM: Staphylococcus epidermidis US-09-134-001C-5581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Acinetobacter baumannii
US-09-328-352-8073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-328-352-8073
                                                                                                                               TYPE: PRT
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Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: LLYND OUGCETE-Stamm et al
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
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Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DEPERMINES FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: DEPERMINES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
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27 ISKINDCFELLAMVTYADFLKGIIKKEFSISFBEFAVLTYISENKEEBYYLKDIINHLNY 86
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                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                     Length 148;
                                                                                                                                                                                                                                                                                                24.9%; Score 143; DB 4; Length 14
29.2%; Pred. No. 8.9e-08;
ive 25; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Mismatches
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5614
LENGTH: 148
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5018
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.2%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.3 Best Local Similarity 28.8 Matches 23; Conservative
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SEQ ID NO 5018
LENGTH: 249
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ORGANISM:
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QD
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Query Match
Best Local Similarity 24.0
Matches 24; Conservative
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US-09-107-532A-6399
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                                                                                                                  16 QVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTK----ALQK 71
                                                                                                                                           |:| :: | :: | :: | :: | 37 QLKHWLKTT---YRISIBEFVVLYKVY--ADTKISGKELRDTLHFEMLWDTSKIDVIIRK 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Indels 15; Gaps
                                                                             <u>ب</u>
                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                   15.4%; Score 88.5; DB 4; Length 136; 27.3%; Pred. No. 0.043; ive 21; Mismatches 42; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 301;
                                                                                                                                                                                             LKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELE 110
                                                                                                                                                                                                                                 IYKKELISKLRSETDERQVYYFFDAKQKKLLDKMTGEIE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION VUMBER: US/08/393,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.7%; Score 84.5; DB 26.1%; Pred. No. 0.32; tive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Dehlinger & Assòciates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 EIEELTYIIKQDINSLNKQIAQLQDFVR 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 LRSESNEISSKEIA----KCSEFKPYY---
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; Sequence 26170, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8600-0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REPERENCE/DOCKET NUMBER: 8600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.13
Matches 23; Conservative
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / MOLECULE TYPE: protein US-08-393-985-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 350 Campa CITY: Palo Alto
                                                        Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
US-09-134-001C-4980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                           RESULT 10
US-08-393-985-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: 1
STATE:
                                                                                                                                                                                             72
                                       Query Match
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
Marc J. Rubenfield et al.
FENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6399, Application US/09107532A
Patent No. 6583275
GENBRAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
14.6%; Score 84; DB 4; Length 368;
Best Local Similarity 28.6%; Pred. No. 0.46;
Matches 26; Conservative 23; Mismatches 40; Indels
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                         TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMER: US/09/252, 991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                             PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-134-001C-3734
; Sequence 3734, Application US/09134001C
; Patent No. 6380370
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USA
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14.5%; Score 83; DB 4; Length 152;
Best Local Similarity 26.4%; Pred. No. 0.19;
Matches 32; Conservative 25; Mismatches 52; Indels
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Patent No. 642023
GENERAL INFORMATION:
APPLICANT: Chang, Sandra
APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
SOFTWARE: ASCII
APPLICATION UNDER: US/09/107,532A
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,51
ATTORNEY/AGENT INFORMATION:
NAME: ATAINEINO: Pamela Deneke
REGISTRATION UNMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
TELEBCOMMUNICATION INFORMATION:
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LOCATION: (B) LÖCATION 1...152

SEQUENCE DESCRIPTION: SEQ ID NO: 6399:

US-09-107-532A-6399
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SEQUENCE CHARACTERISTICS:
                                                                                                                       STATE: Massachusetts
COUNTRY: USA
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122 S 122
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RESULT 15
US-09-134-001C-4421
US-09-134-001C-4421
Patent No. (380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,705
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
14.0%; Score 80.5; Di
Best Local Similarity 23.8%; Pred. No. 1.2;
Matches 36; Conservative 28; Mismatches
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LENCH: 180
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                             ZIP: 10111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRAIN: MAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JACOBS, Seth H
REGISTRATION NUMBER: 32140
REFERENCE/POCKET NUMBER: 1188
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-220
INFORMATION EQ. 10 NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 394 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
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US-09-134-001C-4421

Search completed: November 17, 2003, 12:45:36 Job time: 23 secs

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                                                                                                                                            November 17, 2003, 12:44:45; Search time 267 Seconds (without alignments) 78.630 Million cell updates/sec
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Sequence 4
Sequence 4
Sequence 2
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1 MSKINDINDLVNATFQVKKF......DTQKANIQKLISELEEYIKN
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_TRW PUBL.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_TRW PUBL.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US10NEM_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10NEM_PUB.pep:*
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Compugen Ltd.
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US-10-043-539-2
US-10-043-539-3
US-10-290-143-8
US-10-145-602-4
US-10-043-539-2
US-10-043-539-2
US-10-092-264-4
US-10-092-264-4
US-10-092-264-4
US-10-092-264-2
US-10-092-264-2
US-10-092-264-3
US-10-290-142-4
US-10-290-142-4
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US-10-290-142-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
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GenCore version (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
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Match
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Sequence 2, Application US/10043539;
Sequence 2, Application US/10043539;
Publication No. US20030114650A1;
Sequence 1, Manna, Mabrose;
Sequence 2, Application No. US20030114650A1;
APPLICANT: Cheung, Ambrose;
APPLICANT: Zhang, Gongyi;
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN TITLE OF INVENTION: BACTERA,
ITILE OF INVENTION: BACTERA,
ITILE OF INVENTION: BACTERA,
FILE REFERENCE: DC-019;
CURRENT PILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,637
PRIOR PILING DATE: 2001-01-12
PRIOR PELING DATE: 2001-01-12
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
LENGTH: 115
TYPE: PRI
                    Sequence 5, Appli
Sequence 11, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 746, Appli
Sequence 7611, Appli
Sequence 7611, Appli
Sequence 6808, Appli
Sequence 5, Appli
Sequence 2, Appli
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Sequence 2, Appli
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                                                                                                                                                                                                                                                                           Sequence 5, A
Sequence 7, A
Sequence 7, A
Sequence 7, A
Sequence 3, A
Sequence 3, A
Sequence 3, A
Sequence 3, A
Sequence 2, A
Sequence 2, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Sequence 2, A Sequence 2, A Sequence 1, A Sequence 1, A Sequence 1, A
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US-10-290-143-7

US-10-290-142-5

US-10-290-142-5

US-10-156-741-11146

US-10-290-142-6

US-10-290-143-5

US-10-290-143-5

US-10-022-885-7646

US-09-820-843A-35

US-09-932-1843A-2

US-09-932-1843A-2

US-10-032-585-7611

US-09-932-1843A-2

US-10-057-531A-5

US-10-057-531A-7

US-10-057-532A-7

US-10-057-532A-3

US-10-057-532A-2

US-10-057-532A-2
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100.0%; Pred. No. 4.6e-50;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-043-539-2
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Best Local Similarity 100.0
Matches 115; Conservative
      US-10-043-539-2
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KPYYLTKALOKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN 115

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KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN

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1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYBEIYILNHILRSESNEISSKEIAKCSEF
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                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (77)...(78)
COTHER INFORMATION: "X" is defined as any amino acid residue.
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (86)...(87)
OTHER INFORMATION: "X" is defined as any amino acid residue.
FEATURE:
NAME/KEY: MISC_FEATURE
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LOCATION: (114)..(114)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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NAME/KEY: MISC_FEATURE
LOCATION: (117)...(118)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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; LOCATION: (120)...(120)
; OTHER INFORMATION: "X" is defined as any amino acid residue.
US-10-043-539-26
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LOCATION: (102)...(102)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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LOCATION: (110)..(110)
OTHER INFORMATION: "X" is defined as any amino acid residue.
                                     LOCATION: (58)...(59)
DTHER INFORMATION: "X" is defined as any amino acid residue
                                                                                                                                                                                              LOCATION: (61). (61)

THER INFORMATION: "X" is defined as any amino acid residue
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DIHER INFORMATION: "X" is defined as any amino acid residue
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THER INFORMATION: "X" is defined as any amino acid residue
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THER INFORMATION: "X" is defined as any amino acid residue
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DIHER INFORMATION: "X" is defined as any amino acid residue
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THER INFORMATION: "X" is defined as any amino acid residue
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Best Local Similarity 43.9%; Pred. No. 4.8e-15;
Matches 50; Conservative 15; Mismatches 49;
                                                                                                       FEATURE:
NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC_FEATURE
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US-10-290-142-9
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                                                                                           Sequence 26, Application US/10043539
Publication No. US20030114650A1
GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Manna, Adar
APPLICANT: Chang, Gongyi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
FILE REFERENCE: DC-0199
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LOCATION: (51)..(52)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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OTHER INFORMATION: "X" is defined as any amino acid residue.
FEATURE:
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LUGGATION: (4)...(4)
THER INFORMATION: "X" is defined as any amino acid residue.
FEATURE:
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THER INFORMATION: "X" is defined as any amino acid residue.
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DIHER INFORMATION: "X" is defined as any amino acid residue.
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INFORMATION: "X" is defined as any amino acid residue
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AOCATION: (24)..(25)
THER INFORMATION: "X" is defined as any amino acid
FEATURE:
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OTHER INFORMATION: "X" is defined as any amino acid
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CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,233
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SERVING 26
LENGTH: 120
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OTHER INFORMATION: Consensus sequence.
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NAME/KEY: MISC_FEATURE
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING AGENTS WHICH REGULATE AUTITIES OF INVENTION: PROCESSES IN BACTERIA
FITLE OF INVENTION: PROCESSES IN BACTERIA
FITLE OF INVENTION: PROCESSES IN BACTERIA
FILE REFERENCE: DC-0202
CURRENT APPLICATION NUMBER: US/10/290,143
CURRENT APPLICATION NUMBER: US 10/092,264
PRIOR APPLICATION NUMBER: US 60/329,140
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-08-15
PRIOR PRILING DATE: 2001-08-15
PRIOR PILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-03-06
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: PATENTIN OF VERSION 3.1
SEQ ID NOS: 17
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APPLICANT: McNamara, Peter
TITLE OF INVENTION: REGULATORS OF BACTERIAL VIRULENCE FACTOR EXPRESSION
FILE REFERENCE: KCC 476
CURRENT APPLICATION NUMBER: US/10/145,602
CURRENT FILING DATE: 2002-05-13
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
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3 ITKINDCFELLSMVTYADKLKSLIKKEFSISFEEFAVLTYISENKEKEYYLKDIINHLNY
                                           63 KQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLSRVNKRI 115
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             61 KPYYLTKALQKLKDLKKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
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30.1%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Mismatches
                                                                                                                                                                                     Sequence 8, Application US/10290143
Publication No. US20030124597A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-145-602-4; Sequence 4, Application US/10145602; Publication No. US20030171563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 247
TYPE: PRT
ORGANISM: Staphylococcus aureus
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Best Local Similarity
Matches 30; Conserv
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Sequence 9, Application US/10290142

Publication No. US20030100002A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE

TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE

TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE

CURRENT APPLICATION NUMBER: US/10/290,142

CURRENT FILING DATE: 2002-03-06

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US 60/329,140

PRIOR FILING DATE: 2001-00-15

PRIOR APPLICATION NUMBER: US 60/312,546

PRIOR APPLICATION NUMBER: US 60/273,791

PRIOR FILING DATE: 2001-09-15

PRIOR FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.1

FENDING DE NOS: 15
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Publication No. US20030114650A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Chang, Adar
APPLICANT: Chang, Gongyi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
FILE REFERENCE: DC-0199
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3 ITXINDCFELLSMVIYADKLKSLIKKEFSISFEFFAVLTYISENKEKEYYLKDIINHLNY 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 25.8%; Score 148; DB 15; Length 124; 1 Similarity 30.1%; Pred. No. 2e-07; 34; Conservative 27; Mismatches 52; Indels (
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CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,233
PRIOR FILING DATE: 2001-01-12
PRIOR PELING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR PILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-08
NUMBER: OF SEQ ID NOS: 34
SEQ ID NO 3
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; ORGANISM: Staphylococcus aureus
US-10-290-142-9
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Best Local Similarity
Matches 34; Conserv
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Best Local Similarity
Matches 34; Conserv
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RESULT 9
US-10-043-539-27
US-10-043-539-27
Squence 27, Application US/10043539
Spublication No. US20030114650A1
GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Amana, Adar
APPLICANT: Amana, Adar
APPLICANT: BACTERIA
APPLICANT: APPLICANTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
ITLE OF INVENTION: DACTERIA
FILE REFERENCE: DC-0199
CURRENT APPLICATION NUMBER: US/10/043,539
CURRENT APPLICATION NUMBER: US 60/261,233
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
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PRIOR APPLICATION NUMBER: US 60/289,601
PRIOR DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/289,601
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
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US-10-092-264-4

Squence 4.

Squence 4.

Spublication US/10092264

Spublication No. US2002164761A1

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

FILE REFERENCE: DC-0188

STURENT APPLICATION NUMBER: US/10/092,264

CURRENT APPLICATION NUMBER: US/10/092,264

CURRENT APPLICATION NUMBER: US 60/213,791

PRIOR PILING DATE: 2001-03-06

PRIOR PILING DATE: 2001-03-06

PRIOR PLING DATE: 2001-03-06

PRIOR PRIOR PLING DATE: 2001-03-06

PRIOR PRIOR PLING DATE: 2001-03-06

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M
                                               67 VRALNNLKKOGYLIKERSTEDERKILIHMDDAQODHAEQLLAQVNQLL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 TKALQKIKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 KALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 16.6%; Score 95; DB 15; Length 119; 1 Similarity 21.3%; Pred. No. 0.038; 23; Conservative 29; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
16.3%; Score 93.5; DB 14;
Best Local Similarity 28.4%; Pred. No. 0.062;
Matches 25; Conservative 25; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
US-10-043-539-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 23; Conserv
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APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
APPLICANT: Anna, Adar
APPLICANT: Anna, Gongyi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
TITLE OF INVENTION: BACTERIA
FILLE REFERENCE: DC-0199
CURRENT APPLICATION NUMBER: US/10/043,539
CURRENT PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR PLING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 34
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Sequence 2, Application US/10145602
PUBlication No. US2030171563A1
GENERAL INFORMATION:
PUBLICATION:
PAPPLICANT: WORMERAY
THE OF INVENTION: REGULATORS OF BACTERIAL VIRULENCE FACTOR EXPRESSION
FILE REFERENCE: KCC 476
CURRENT APPLICATION NUMBER: US/10/145,602
CURRENT FILING DATE: 2000-05-13
PRIOR APPLICATION NUMBER: US 60/291,917
PRIOR APPLICATION NUMBER: US 60/291,917
PRIOR PLING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
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                                               KALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.9%; Score 120; DB 12; Length 166; 28.0%; Pred. No. 0.00018; tive 26; Mismatches 45; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.0%; Score 115; DB 15; Length 118;
25.0%; Pred. No. 0.00037;
live 26; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Sequence 28, Application US/10043539
, Publication No. US20030114650A1
, GENERAL INFORMATION:
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US-10-145-602-2
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Best Local Similarity 28.0%
Matches 33; Conservative
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US-10-043-539-28
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LENGTH: 166
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Best Local S
Matches 27
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us-10-043-539a-2.rapb

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Sequence 2, Application US/10290142
; Publication No. US20030100002A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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; Publication No. US20030124597A1
; Publication No. US20030124597A1
; Publication No. US20030124597A1
; Publication No. US20030124597A1
; APPLICANT: Cheung, Ambrose
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING AGENTS WHICH REGULATE AUT.
; TITLE OF INVENTION: PROCESSES IN BACTERIA
; FILE OF INVENTION: PROCESSES IN BACTERIA
; FILE REFERENCE: DC-0202
; CURRENT APPLICATION NUMBER: US/10/290,143
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/329,140
; PRIOR PILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/312,546
; PRIOR PAPLICATION NUMBER: US 60/273,791
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                               15 LYNAQRQVNRYYSNKVFKKYNLTYPQFLVLT-ILWDES-PWNVKKVVTELALDTGTVSPL 72
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                Length 147;
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        Query Match
16.3%; Score 93.5; DB 14;
Best Local Similarity 28.4%; Pred. No. 0.069;
Matches 25; Conservative 25; Mismatches 35;
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|::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
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US-10-290-143-3
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Sequence 4, Application US/10290142

Sequence 6, Application US/10290142

Sequence 6, Application US/10290142

SETERAL INFORMATION:

APPLICANT: Cheung, Ambrose

TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE

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FRICK PELICATION NUMBER: US 60/329,140

PRIOR PILING DATE: 2001-10-12

PRIOR PILING DATE: 2001-08-15

PRIOR PILING DATE: 2001-08-15

PRIOR FILING DATE: 2001-03-06

NUMBER FOR SEQ ID NOS: 15

SECTWARR: PAPENTIN VERSION 3.1

FEMALE OF SEQ ID NOS: 15

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Publication No. US20020164761A1

Publication No. US20020164761A1

REDEREAL INFORMATION:
APPLICANT: Trustees of Dartmouth College
TITLE OF.INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN BA
FILE REPRENCE: DC-0188

CURRENT FILING DATE: 2002-03-06

PRIOR PELING DATE: 2001-03-06

PRIOR FILING DATE: 2001-03-16

PRIOR PEPLICATION NUMBER: US 60/273,791

PRIOR PEPLICATION NUMBER: US 60/312,546

PRIOR PEPLING DATE: 2001-08-15

PRIOR PEPLING DATE: 2001-08-15

PRIOR PEPLING DATE: 2001-08-15

PRIOR SPELING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 4
                                                                                                            15 LYNAQRQVNRYYSNKVFKKYNLTYPQFLVLT-ILWDES-PVNVKKVVTELALDTGTVSPL 72
LVNATFQVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LVNATFQVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA 68
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16.3%; Score 93.5; DB 15; Length 134;
Best Local Similarity 28.4%; Pred. No. 0.062;
Matches 25; Conservative 25; Mismatches 35; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                      |:::: : |:::| |:| |:| |:| |:| |:::| | |:::| | |:::| | |:::| | |:::| | |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:
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; ORGANISM: Staphylococcus aureus
US-10-290-142-4
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CRGANISM: Staphylococcus aureus
US-10-092-264-2
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Sequence 8, Application US/10290142

Sequence 8, Application US/10290142

Publication No. US20030100002A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: DC-0195

CURRENT FILING DATE: 2002-11-06

PRIOR PILING DATE: 2002-03-06

PRIOR PAPLICATION NUMBER: US 0/092, 264

PRIOR PILING DATE: 2001-10-12

PRIOR PILING DATE: 2001-10-12

PRIOR PILING DATE: 2001-10-12

PRIOR PILING DATE: 2001-00-15

PRIOR FILING DATE: 2001-00-15

PRIOR FILING DATE: 2001-00-15

PRIOR FILING DATE: 2001-00-15

PRIOR FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PARCHILING VERSION 3.1

LEASTHAND BELLING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PARCHILING VERSION 3.1

LEASTHAND BELLING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PARCHILING VERSION 3.1

LEASTHAND BELLING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PARCHILING VERSION 3.1
                                                                                                                                                                                                                                                                                                                         10 LUNATFQVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA 68
                                                                                                                                                                                                                                                                                                                                                              16.3%; Score 93.5; DB 15; Length 147; 28.4%; Pred. No. 0.069; Live 25; Mismatches 35; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.9%; Score 91; DB 15; Length 153; ilarity 26.4%; Pred. No. 0.13; Conservative 21; Mismatches 44; Indels
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73 LKRMEQVDLIKRERSEVDQREVFIHLTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                           69 LOKLKDLKLLSKKRSLQDERTVIVYVTD 96
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                                                                                      TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-290-143-3
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 147
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Best Local Similarity 28.4%
Matches 25; Conservative
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10 LVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKAL 69

Search completed: November 17, 2003, 12:54:10 Job time: 267 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 17, 2003, 12:36:25; Search time 25 Seconds (without alignments) 442.376 Million cell updates/sec Run on:

Title: Perfect score:

US-10-043-539A-2 574 1 MSKINDINDLVNATFQVKKF.....DTQKANIQKLISELBEYIKN 115 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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probable transcrip	<pre>probable transcrip</pre>	KLP2 protein - Afr	transcription regu	hypothetical profe	signal-transducing	DNA-directed DNA p	hypothetical prote	myosin-like protei	hypothetical prote	probable transcrip	DNA-directed DNA p	hypothetical prote	M6R protein - vari	major merozoite su	probable major sur
E98132	D83290	T30335	AC1720	E90291	B69439	S25855	A64465	S38173	H90260	B95400	D64246	T34567	A72161	805603	A24594
	7	N	C)	N	N	N	N	(7)	Ŋ	7	C)	N	C/I	(7)	C)
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150 2	151 2	1388	150	144	338	964	1005				260	.2 755	.2 1286	.2 1639	2
150 2	73	1388	150	144	338	964	1005				260	.2 755	.2 1286	1639	2
150 2	4 14.6 151 2	1388	3 14.5 150	14.4 144	14.4 338	14.4 964	14.4 1005	14.4		14.3	14.2 260	14.2 755	14.2 1286	.2 1639	14.2

## ALIGNMENTS

RESULT 1 B90028 b90028 c)Species: C)Species: C)Accessio R)Kucces ma, A, Mi C) C, Shiba	RESULT 1 By0028 By0028 By0028 By0028 C;6pecies: Staphylococcus aureus C;6pecies: Staphylococcus aureus C;6pecies: Staphylococcus aureus C;0pecies: Dougles: 10. May-2001 By0028 C;0pecies: By0028 By0028 By0028 By0028 By0028 By0028 By0028 By0028 By1038 By10
A, Title: Who A, Reference A, Accession: A, Status: pr A, Molecus: pr A, Residues: A, Cross-refe A, Experiment C, Genetics: A, Gene: sarR	A. Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A. Reference number: A89758; MUID:21311952; PMID:11418146 A. Accession: B90028 A. Accession: B90028 A. Molecule type: DNA A. Residues: 1-115 < KUR> A. Residues: 1-115 < KUR> A. Residues: 1-115 < KUR> A. Residues: 1-115 < KUR> A. Residues: GB:BA000018; PID:g13702095; PIDN:BAB43387.1; GSPDB:GN00149 A. Experimental source: strain N315 C. Genetics: A. Genetics:
Query Match Best Local Matches 11	Ouery Match 100.0%; Score 574; DB 2; Length 115; Best Local Similarity 100.0%; Pred No. 7.3e-40; Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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	0; Mismatches 0; Indels 0; Gaps C	1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEBIYILNHILRSBSNBISSKBIAKCSBF 60
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Query Match Best Local Similarity	Matches 115; Conservative	
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staphylococcal accessory regulator A [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001
C;Accession: B89831
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Iancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: B89831
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <CUL>
A;CUR>
A;Cross-references: GB:BA000018; PID:g13700508; PIDN:BAB41805.1; GSPDB:GN00149
A;Experimental source: strain N315

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Gaps

A;Gene: sarA C;Genetics:

Matches

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hypothetical protein sarH1 [imported] - Staphylococcus aureus (strain N315) C, Species: Staphylococcus aureus (species: Staphylococcus aureus (species: Staphylococcus aureus (species: Staphylococcus aureus (species: 10-May-2001 #sequence_revision: 10-May-2001 #text_change 22-Oct-2001 C, Edate: 10-May-2001 #sequence_revision: 10-May-2001 #text_change 22-Oct-2001 C, Exturcda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A, Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A, Reference number: A, May MulD:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #text_change 22-Oct-2001
C;Accession: F90024
R;Kuroda, M.; Ohte, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-250 cKUR>
A;Cross-references: GB:BA000018; PID:g13700028; PIDN:BAB41327.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: sarH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:BA000018; PID:g13702067; PIDN:BAB43359.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146
                                                          7 INDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 DINDLVNATFQVKKFFRDTKKKFNLNYEELYILNHILRSESNEISSKEIAKCSEFKPYYL 65
                                                                                                              9 VNKFINVEAXIFFLTQELKQQYKLSLKELLILAYFYYKNBHSISLKEIIGDILYKQSDVV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 QVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTK----ALQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein [imported] - Staphylococcus aureus (strain N315)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.0%; Score 115; DB 2; Length 250; 25.0%; Pred. No. 0.025; ive 26; Mismatches 55; Indels
   Indels
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52;
   Mismatches
   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.0%
Matches 27; Conservative
      Conservative
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Matches 29; Conserv
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A,Status: preliminary
A,Molecule type: DNA
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A, Status: preliminary
A, Molecule type: DNA
      30;
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      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. Species: Staphylococcus aureus (strain N315)
C. Species: Staphylococcus aureus
C. Date: 10-May-2001 #text_change 22-Oct-2001
C. Species: Other 2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C. Accession: F89961
M.; Other, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUD:21311952; PMID:11418146
A; Accession: F89561
A; Residues: Dreliminary
A; Molecule type: DNA
A; Residues: 1-153 acvus
A; Residues: 1-153 acvus
A; Cross-references: GB:BA000018; PID:g13701558; PIDN:BAB42851.1; GSPDB:GN00149
A; Experimental source: strain N315
C; Genetics:
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D90053
hypotherical protein sarH2 [imported] - Staphylococcus aureus (strain N315)
c,Species: Staphylococcus aureus
C,Species: Staphylococcus aureus
C,Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C,Accession: D90053
F, Uchtoda, M.; Obfa, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Minutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 201
A,7title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A,Reference number: A89758; MUID:21311952; PMID:11418146
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A;Residues: 1-247 <KUR>
A;Cross-references: GB:BA000018; PID:g13702449; PIDN:BAB43590.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                     1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKINDINDLVNATFQ-----VKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 MKKVN--NDTVFGILQLETLLGDINSIFSEIESEYKMSREBILIL--LTLWQKGSMTLKE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 IAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTD----TQKANIQKLISE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI
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                                                                                              25.8%; Score 148; DB 2; Length 124; 30.1%; Pred. No. 2.5e-05;
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                                                                                                                                                           Mismatches
                                                                                                                                                     27;
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27.8%;
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Best Local Similarity 28.05
Matches 33; Conservative
                                                                                                                                                        34; Conservative
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Best Local Similarity
                                                                                                                                 Best Local Similarity
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A; Status: prelimina:
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C,Accession: D86889
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Ress. 11, 731-753; 2001
A;Title: The Complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                           - Lactococcus lactis subsp. lacti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: G89839
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Tile: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Cross-references: GB:AE005176; PID:g12725171; PIDN:AAK06214.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SA0641 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                    zinc transport transcription regulator zitR [imported] - Lactococcus lactis C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LYNAQRQVNRYYSNKVFKKYNLTYPQFLVLT-ILWDES-PVNVKKVVTELALDTGTVSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSLANQIDQFLGTIMQ----FAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKCSEPKPYYLTKALQKLKDLKLLSKKRSLQDERTVI------VYVTDTQKANIQKLIS
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16.3%; Score 93.5; DB 2;
Best Local Similarity 27.4%; Pred. No. 0.76;
Matches 34; Conservative 23; Mismatches 50;
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llarity 28.4%; Pred. No. 0.77;
Conservative 25; Mismatches 35;
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89 TVIVYVTDTQKANIQKLISELE 110
                                       95 AVVLTITEKGNSVYEECEKQLE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 25; Conserv
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A;Molecule type: DNA
A;Residues: 1-147 <KUR>
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A, Status: preliminary
A, Molecule type: DNA
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Matches
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                                                                                                                                                                                                                                                  regulatory proteins (Mark Family) homolog lmo0989 [imported] - Listeria monocytogenes (s C) Species: Listeria monocytogenes C; Species: Listeria monocytogenes C; Species: Listeria monocytogenes C; Species: Listeria monocytogenes C; Species: Listeria monocytogenes C; Species: Listeria monocytogenes C; Species: 27-Nov-2001 (s) Accession: AE198 (s) Accession: AE198 (s) Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001 (s) Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tiereria species. Madueno, E.; Maitournam, A.; Maccession: AE1198 (s) Mulb:21537279; PMID:11679669 (s) Accession: AE1198 (s) Mulb:21537279; PMID:11679669 (s) Mulb:21537279; PMID:21537279;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription regulator (MarR family). homolog lin1188 [imported] - Listeria innocua (St Species: Listeria innocua (Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #sequence_revision 27-Nov-2001 (Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 (Species: P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. D.; Varander, E.; Maitournam, A.; Marchinors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Macker (C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Mehland, A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: Acidsulary
A; Molecule type: DNA
A; Residues: 1-150 < GLAs
A; Cross-references: GB:ALS92022; PIDN:CAC96419.1; PID:g16413647; GSPDB:GN00178
A; Experimental source: strain Clip11262
C; Genetics:
A; Genetics:
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16.4%; Score 94; DB 2; Length 150;
Best Local Similarity 24.4%; Pred. No. 0.72;
Matches 20; Conservative 27; Mismatches 33; Indels
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                                                                 LKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELE 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Mismatches
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Oguc K.;

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Wypotherical protein BB0512 - Lywe disease spirochete
C;Species: Borrelia burgdorferi (Lywe disease spirochete)
C;Decies: Borrelia burgdorferi (Lywe disease spirochete)
C;Date: 13-F6-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Accession: G70163
R;Fraser C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Rerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Sowman, C.; Garland, S.; Fujli, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Athorescon: G70163
A;Accession: G70164
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A;Accession: G70165
A;
                                                                                                                                                                                                            R;Ito, M.; Cooperberg, B.; Krulwich, T.A. submitted to the EMBL. Data Library, February 1997
A;Description: Cloning and sequencing of Na+/H+ antiporter homolog gene from alkaliphilic
A;Reference number: Z26111
A;Accession: T52550
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Species: Listeria innocua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Bacillus firmus
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Mar-2002
C;Accession: T52550
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                                                                                      probable transcription regulator 16.1K [imported] - Bacillus firmus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-148 <ITO>
A;Cross-references: EMBL:U99914; PIDN:AAB87745.1
A;Experimental source: strain OF4
C;Superfamily: transcription regulator yfiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
15.8%; Score 90.5; DE
Best Local Similarity 26.5%; Pred. No. 1.4;
Matches 26; Conservative 24; Mismatches
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Best Local Similarity 32.2%
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         Clo
                                                                                                                                                                                                                                                                                               R.; Lee
                                                                                                                                                 Appase involved in DNA repair [imported] - Clostridium acetobutylicum Cj9/230 Appase involved in DNA repair [imported] - Clostridium acetobutylicum CjSpecies: Clostridium acetobutylicum CjSpecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 CjAccession: G9720 Apparent, G.v.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Le Jally, M.G.; Benett, G.v.; Koodin, E.V.; Smith, D.R. Apparented and Comparative Analysis of the Solvent-Producing Bacterium CA; Reference number: A96900; MUD:21359325; PMID:21359325 Apparented preliminary Apparented Europe: DNA Apparented Europe: DNA Apparence and Comparative Apparence and Capparence and Capparence and Capparence and Capparence Apparence and Capparence Apparence Clostridium acetobutylicum ATCC824
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Residues: 1-247 <KUR>
Cross-references: GB:BA000018; PID:gl3702097; PIDN:BAB43389.1; GSPDB:GN00149;
Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYVSYLLSSQELFRNLKCYLNMCQLTLEELYVLG-ILNLHKGQLTVKELQ--GEFHHPIF 186
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LKRMEQVDLIKRERSEVDQREVFIHLTD 100
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Matches 33; Conserv
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Matches 36, Conser
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A;Experimental sc
C;Genetics:
A;Gene: CAC2736
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A, Experimental
C, Genetics:
A, Gene: SA2091
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: ACISS6
R;Glascr, Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
.; Domingue, P.; Frangeul, L.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-882, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Ma
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Alticle: Comparative genomics of Listeria species.
A;Accession: ACISS6
A;Accession: ACISS6
A;Accession: ACISS6
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-141 <GLA>
A;Cass-references: GB:AL522022; PIDN:CAC96219.1; PID:g16413447; GSPDB:GN00178
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
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15.4%; Score 88.5; DB 2; Length 141;
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 25; Conservative 26; Mismatches 48; Indels 1
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Search completed: November 17, 2003, 12:45:08 Job time : 28 secs

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P13819 plasmodium P08569 plasmodium P04934 plasmodium P50495 plasmodium Q02224 homo sapien 067642 aquifex aeo 060563 mesocricetu Q65209 mus musculu P59037 methanococc P19598 plasmodium P52611 borrelia bu Q8d2w@ wiggleswort

MSP1\_PLAFF MSP1\_PLAFM MSP1\_PLAFF MSP1\_PLAFP CENE\_HUMAN TTT\_AQUAE SCP1\_MOUSE S

ALIGNMENTS

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November 17, 2003, 11:25:47; Search time 15 Seconds (without alignments) 360.538 Million cell updates/sec
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574
1 MSKINDINDLVNATFQVKKF......DTQXANIQKLISELBEYIKN 115
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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EXSB_BORBU
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., A Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., A Johnston M., Andrews S., Brinkman R., Gorco T., Kirsten J.,

Kucaba T., Hallsworth K., Hawkins J., Hillier I., Jier M.,

A Mardis E., Menezes S., Miller N., Nan M., Pauley A., Peluso D.,

A Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,

A Rifken L., Rales L., Taich A., Trevaskis E., Vignati D.,

A Nilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;

E. Submitted (MAR.1996) for the BMBL/GenBank/DBJ derabases.

C. -- FUNCTION: REQUIRED FOR MILOTIC CHROMOSOME SYNAPSIS AND

C. -- PROGRESSION. MAY ACT AS A MOLECULAR ZIPPER TO BRING HOWOLOGOUS

C. CHROMOSOMES IN CLOSE APPOSITION. ZIPPER TO BRING HOWOLOGOUS

C. SUBCELLULAR LOCATION: SYNAPSED MEIOTIC CHROMOSOMES.
                                                                                         873 KVNDI-DKLNKILMEEKFENIEKAKENYLNDKEINLLKSDVEKYKNELSKVNGA----- 925
                                                       PYYLTKALQKLKDLKLLSKK---RSLQDERTVIVYVTDTQKANIQKLISE----LEEYIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sym M., Engebrecht J.A., Roeder G.S.; "ZIP1 is a synaptonemal complex protein required for meiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 34, Last sequence update) (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            875 AA.
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Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synaptonemal complex protein ZIP1.
ZIP1 OR YDR285W OR D9819.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BR1824-3B;
MEDLINE=93161412; PubMed=7916652;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72:365-378(1993)
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Best Local Similarity

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                                                                          677
                                                                                                                                            8 NDLVNATFOVKKFFRDTXKKFNLNYEBIYILNHILRSESNBISSKBIAKCSBFKPYYLTK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfan, PP00580; UvrD-helicase; 1.
TIGRFAMS; TIGR0609; recB; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.K., Quackenbush J., Salzberg S., Hanson M., Utterback T., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Wathey L., McDonald L., Artiach P., Bowman C., Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Vener J.C.,
                                                                          621 NEOKDHTTKLEAFOKNNEOLOKLNVEVVOLKAHELELEE---ONRHLKNCLEKKETGVEE
                                                                                                                   ----LLSKKRSLQDERTVIVYVT-----DTQKANIQKLISE
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'- to 3'-or 3'- to 5'-direction to yield 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         burgdorferi.";
Nature 390:580-586(1997).
-!- FUNCTION: REDUIRD FOR EFFICIENT DNA REPAIR; IT CATALYZES THE
-!- UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-
STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.
ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP
(BY SIMILARITY).
23;
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-!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphooligonucleotides.
SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
Indels
46;
                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2000 (Rel. 39, Last sequence update)
Exodeoxyribonuclease V beta chain (BC 3.1.11.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA repair, Complete proteome.
NP BIND 18 25 ATP (POTENTIAL).
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed=9403685;
26;
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30-MAY-2000 (Rel. 39, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001164; AAC66981.1; -. PIR; H70178; H70178.
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TIGR, BB0633, -
InterPro, IPR004586; RecB.
InterPro, IPR000212; UvrD-
Conservative
                                                                                                                     68 ALQKLKDLK----
                                                                                                                                                                                                  109 LEEYIKN 115
                                                                                                                                                                                                                                        738 LEE-IKN 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            296 DNRNKNR-----NNLKQYVILKVEYKILKYIEKELKKTIKSTNTIDQNYIISNLKNYLKS 350
                                                                            237 SKENDIFKIAE-TLLKNKFFSTLIEKETKKOSKLSPKELKIKNDLICLGINIKHEKYKSE 295
                                                                                                46 SNEISSKEIAKCSEFKPYYLTKALQKL-----KDLKLLSKKRSLQDERTVIVYVTDTQKA 100
                                                          45
                                                                                                                                                                                                                                                                                                                                            Syntaa.....
SYNTAA OK SIXIS.
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
ANCHOR FOR TYPE IV MEMBRANE PROTEIN (POTENTIAL).
VESICULAR (POTENTIAL).
COLLED COLL (POTENTIAL).
T.SHARE COLLED-COLL HOMOLOGY.
T. F560ALA079C8A9F7 CRC64,
                                       27;
                   DB 1; Length 1169;
                                                         2 SKINDINDLVNATFQVKKFF-----RDTKKKFNLNYEEIYILNHIL--
                                       Indels
B61D63C1C959B91F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coiled coil; Transmembrane; Transport; Golgi stack.
DOMAIN 1 279 CYTOPLASMIC (POTENTIAL
                                      48;
                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                  ; Score 85.5; DB
; Pred. No. 16;
26; Mismatches
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InterPro; IPR006012; Syntaxin.
InterPro; IPR006011; Syntaxin.N.
InterPro; IPR00077; T SNARE.
Pfam; PF00804; Syntaxin; 1.
SNART; SM00397; T SNARE; 1.
PROSITE; PS00914; SYNTAXIN; 1.
PROSITE; PS00914; SYNTAXIN; 1.
137828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34117 MW;
                   14.9%;
24.6%;
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                                                                                                                                      101 NIOKLISELEEYIK 114
                                                                                                                                                   351 EDKKLINAIKNRYK 364
             Query Match
Best Local Similarity 24.68
                                                                                                                                                                                                          STANDARD;
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1169 AA;
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85
209
301 AA;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=Brain;
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DOMAIN
SEQUENCE
SEQUENCE
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-!-SUBUNIT: Consists of at least two heavy chains and a number of intermediate and light chains.
-!-DOMAIN: Dynain heavy chains probably consist of an N-terminal stem (which binds cargo and interacts with other dynain components), and the head or motor domain. The motor contains six tandemly-linked AAA domains in the head, which form a ring. A stalk-like structure (formed by two of the coiled coil domains) protrudes between AAA 4 and AAA 5 and terminates in a microtubule-binding site. A seventh domain may also contribute to this ring; it is not clear whether the N-terminus or the C-terminus forms this extra domain. There are four well-conserved and two non-conserved ATPase sites, one per AAA domain. Probably only one of these (within AAA
                                                                                                                                                                                                                  TISSUE=Nasal polyps;
Maiti A.K., Mattei M.-G., Jorissen M., Volz A., Ziegler A.,
Bouvagnet P.,
Chromosomal localization of human dynein heavy chain genes.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Force generating protein of respiratory cilia. Produces
force towards the minus ends of microtubules. Dynein has ATPase
activity; the force-producing power stroke is thought to occur on
release of ADP.
                                                                                                                                                                   42 LRSESNEISSKEIA----KCSEFKPYY-----LTKALQKLKDLKLLSKKRSLQDERTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] SEQUENCE FROM N.A., VARIANT PCD GLN-3004, AND VARIANTS LEU-34; SEQUENCE FROM N.A., VARIANT PCD GLN-3004, AND VARIANTS LEU-34; VAL-3715; PRO-3765 AND ILE-4177.
TISSUE-ansaal epithelium, and Testis; MEDLINE-22155903; PubMed-12142464; MEDLINE-22155903; PubMed-12142464; Ghrig C., Maiti A.K., Scamuffa N. Bartoloni L., Blouin J.L., Pan Y., Gehrig C., Maiti A.K., Scamuffa N., Rossier C., Jorissen M., Armengot M., Meeks M., Mitchison H.M., Chung E.M., Delozier-Blancher C.D., Craigen W.J., Antonarakis S.E.; "Mutations in the DNAHII (axonemal heavy chain dynein type 11) gene cause one form of situs inversus totalis and most likely primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: Defects in DNAH11 are a cause of immotile cilia syndrome
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           096075; 09UJ82;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last saquence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ciliary dynein heavy chain 11 (Axonemal beta dynein heavy chain 11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          actually hydrolyzes ATP, the others may serve a regulatory
                                                                                     15;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sterility.
-!-:SIMILARITY: Belongs to the dynein heavy chain family.
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Proc. Natl. Acad. Sci. U.S.A. 99:10282-10286(2002)
                                                                                 27;
DB 1;
; Score 84.5; DE; DE; Pred. No. 4.6; 23; Mismatches
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                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Query Match
Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                               InterPro; IPR003593; AAA ATPase.
InterPro; IPR005613; AIP3.
InterPro; IPR004273; Dynein_heavy.
Pfam; PF03028; Dynein heavy; I.
SMART; SM00382; AAA; 4
Motor procein; Dynein; Microtubules; ATP-binding; Repeat; Coiled coil;
DoMAIN; I lease mutation.
STEM (BY SIMILARITY).
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|FTIG=VAR 013863.
| 7C9A7IC95B296B89 CRC64;
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AAA 2 (BY SIMILARITY).
AAA 3 (BY SIMILARITY).
AAA 4 (BY SIMILARITY).
AAA 6 (BY SIMILARITY).
AAA 6 (BY SIMILARITY).
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COLLED COIL (POTENTIAL).
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COLLED COIL (POTENTIAL).
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'FTId=VAR_013854.
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FTId=VAR_013861.
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FTId=VAR_013855.
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'FTId=VAR_013852
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/FTId=VAR_013856.
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/FTId=VAR_013862
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FTId=VAR_013853
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ATP (POTENTIAL)
ATP (POTENTIAL)
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                                                                              EMBL; AJ320497; CAC60121.1; -. EMBL; AJ132087; CAA10560.1; -. Genew; HGNC:2942; DNAH11.
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Best Local Similarity
Matches 32; Conserv
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MIM; 603339;
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NP BIND
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                            3108 NGIQKLKTTASQVGDLKARLASQEAELQLRNHDAEALITKIGLQTEKVSREKTIADAEE 3166
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67 KALQKLK-----DLK--LLSKKRSLQ----DERTVIVYV-TDTQKANIQKLISELEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SKINDINDLVNATFQVKKF----FRDTK-----KKFNLNYEBIYILNHILRSESNBISSK 52
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92199242; PubMed=1840516;
Mustafa A., Yuben L.;
Mustafa A., Yuben L.;
"Identification and sequencing of the Choristoneura biennis entomopoxvirus DNA polymerase gene.";
DNA Seq. 2:39-45(1991).
-!- CATALYMIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + {DNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                           01-APR.1993 (Rel. 25, Created)
01-APR.1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7)
Chorsistoneura biennis entomopoxvirus (CbEPV):
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirus B.
NCBI_TAXID=10288;
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-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; DNA-directed DNA polymerase; DNA replication;
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                                                                                                                          964 AA
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(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X57314; CAA40566.1; -.
PIR; S25855; S28855.
InterPro; IPR006172; DNA_DOL_B.
InterPro; IPR006134; DNA_DOL_B dom.
InterPro; IPR006133; DNA_DOL_B exo.
Pfam; PF00136; DNA_DOL_B exo; Pfam; PF03104; DNA_DOL_B exo; 1.
SNART; SM00486; POLES; 1.
PROSITE; PS00116; DNA_POLYMERASE_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 EYIKN 115
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ID RASO METJA
AC QS8718;
DT 16-OCT-2001 ()
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                          CBEPV
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Best Local S
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                                                                                       RESULT 6
DPOL_CBEPV
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STRAIN-S288C;
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   OPTHER NO DOUGH THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 ILEYDLNTVVEARETLNRHKDEYEKYKSLVÖEIRKI-----ESRLRELKSHYEDYLK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ALL-I, DSM 2661 / ATCC 43067;
MDDINB=96337999; Pubmed=8686887;
Bult C.J., White O., Olsen G.J., Zhou L., Fletschmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fletschmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayron R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoglagen N.S.M., Weidman J.F., Pihrmann J.L.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
"Complete genome sequence of the methanogenic archaecn, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 273:1058-1073(1996).

-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KINDINDLVNATFQVKKFFRDTKKKFN-----LNYEBIYILNHILRSBSNBISSKBIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.4%; Score 82.5; DB 1; Length 1005; 29.4%; Pred. No. 24; .ive 25; Mismatches 40; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Forms a complex with mre11 (By similarity).
-!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1005 AA; 119387 MW; 9BBBB48173E788F3 CRC64;
                                                                                                                                            Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
28-FEB-2003 (Rel. 41, Last annotation update)
DNA double-strand break repair rad50 ATPase.
MAD50 OR M11322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TICK, M01322, --
HAWAP; ME 00449; --; 1.
HAWAP; MF 00449; --; 1.
InterPro: IPR003439; AAA_ATPase.
InterPro: IPR003405; SMC_C.
InterPro: IPR003405; SMC_N.
Pfam; PF04423; SMC_C, 1.
Pfam; PF02443; SMC_C, 1.
ProDom: PF00406; ABC transporter; 1.
SMART; SM00382; AAA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67572; AAB99331.1; -.
                                                                                                            Methanococcus jannaschii.
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Matches 35; Conserv
                                                                                                                                                                                                                      NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
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STITE BY A REPLY A REP
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1875 AA.

PRT;

STANDARD;

RESULT 8 MLP1\_YEAST ID \_MLP1\_YEAST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 BPKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISE-LEEYIKN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 NDINDLVNATFQVKKFFRDTKKKF-----NLNYBEIYILNHILRSESNEISSKEIAKCS
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MEDINE-94205265;

MEDINE-94205265;

MEDINE-94205265;

MEDINE-94205265;

MEDINE-94205265;

MEDINE-94205265;

MEDINE-9506,

MEDINE-9506,

MEDINE-9506,

MEDINE-9506,

MEDINE-9606,

ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: MYOSIN-LIKE PROTEIN THAT IS PROBABLY INVOLVED IN DNA
                                                                                                                               Myosin-like protein M.Pl.
MLP1 OR YKR055W OR YKR415.
Saccharonyces cerevisiae (Baker's yeast).
Bukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93247549; PubMed=8483450;
Koelling R., Nguyen T., Chen B.Y., Botstein D.;
"A new yeast gene with a myosin-like heptad repeat structure.";
Mol. Gen. Genet. 237.359-369(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
(R -> A [IN REF. 1).
(W, 683A0D34C9066867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: SOME, TO THE TPR ONCOGENE.
-!- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO: GO: 0005635; C:nuclear membrane; IDA.
GO: GO: 0005654; C:nucleoplasm; IDA.
GO: GO: 0006606; P:protein-nucleus import; IDA.
01-OCT-1993 (Rel. 27, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Æ
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(Rel. 33, Last sequencé update)
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EMBL; X73541; CAA51948.1; -.
EMBL; Z28320; CAA82174.1; -.
PIR: S1817.
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Best Local Similarity 28.8
Matches 34, Conservative
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DOMAIN 69 487
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SGD; S0001803; MLP1.
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1875 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
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P47659;
01-FEB-1996
01-FEB-1996
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ID DP3X_M
AC P47659
DT 01-FEB
DT 01-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 LFIFTTTEFNKÍPLTILSRCQSFFFKKITSDLILERLND----IAKKEKIKIEKDALIKIA 206
                                                                                                                                                                                                                                                                                                                                The minimal gene complement of Mycoplasma genitalium.", Science 270:397-403(1995).
-!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR THE REPLICATIVE SYNTHESIS IN BACTERIA.
THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This core dimerizes to form the POLIII' complex. PolIII' associates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).
                                                                                                                                        SEQUENCE FROM N.A.
STRAINCATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fraser C.M., Gocayne J.D., White O., Rerlayage A.R.; Sutton G., Kelley J.M.,
Fleischmann R.D., Bult C.J., Kerlayage A.R.; Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougharty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NEISSKEIAKCSE--FKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVT
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                                                                                   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART, SM00382, AAA, 1.
Transferase, DNA-directed DNA polymerase, DNA replication,
ATP-binding, Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 51 ATP (POTENTIAL).
260 AA; 29772 MW; 80908B0FID6D78D4 CRC64;
28-FEB-2003 (Rel. 41, Last annotation update) DNA polymerase III subunit gamma (EC 2.7.7.7) DNAX OR DNAH OR MG420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.2%; Score 81.5; DE 22.8%; Pred. No. 6.9; iive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro, IPR003593; AAA ATPase.
Interpro, IPR003959; AAA ATPase centr.
Interpro, IPR00862; RFCGomain.
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P04932;
13-AUG-1987 (Rel. 05, Created)
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PIR; D64246; D64246.
TIGR; MG420; -.
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                                                                  Mycoplasma genitalium.
                                                                                                          NCBI_TaxID=2097;
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SEQUENCE
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MSP1_PLAFK
ID MSP1_PL
AC P04932;
DT 13-AUG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Indels 33; Gaps
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                    -!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS O MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                MEDLINE-86136024; PubMed=3004972; Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Katunenberg H., Bujaxd H.; Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006209; BGF_like.
Pfam; PF00008; EGF; 1.
Malaria; Merozolte; Polyprotein; Repeat; Signal; Glycoprotein; Transmembrane; GFI-andor.
SIGNAL 1 19
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(POTENTIAL)
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                                                                          Plasmodium falciparum (isolate K1 / Thailand).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN 1.
                                                                                                                                                                                                                                                         REVISIONS, SEQUENCE FROM N.A.
Pan W., Tolle R., Bujard H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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MERCOCITE SURFACE PI
MEMBRANE ANCHOR.

N-LINKED GLCNAC.

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Pred. No. 49
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1630
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1165
1436
1517
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                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                           NCBI_TaxID=5839;
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1165
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                                             (PMMSA) (P190)
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TRANSMEM
CARBOHYD
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CARBOHYD
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Best Local
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                                                                                                                                                                                                  Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T., Freeman R.R.;
                                                                                                                                                                                                                                                                                                                                                            -1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                                                                                                                                                                                                                                                                                                            Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
                                               13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (P195).
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                                                                                                                                                                                                                                           "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A24594; A24594.
PIR; S05603, S05603.
INTERPRO, IPRO06209; EGF_like.
PERM: PF000008; EGF_like.
Pfam: PF000008; EGF_like.
Transmembrane; GP1-anchor; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81.5; DB 1; Length 1639;
Pred. No. 49;
                                                                                                          Plasmodium falciparum (isolate Wellcome).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5848;
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N-LINKED (GLCNAC.
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(GLCNAC.
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                        1639 AA
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                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=86014355; Pubmed=2995820;
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Best Local Similarity 25.4
Matches 35; Conservative
                        STANDARD;
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116
268
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920
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1526
1639
                        PLAFW
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CARBOHYD
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                          MSP1 PI
P04933;
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RESULT 11
MSP1_PLAFW
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52

NATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSK

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OR RAF GENES.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/TPRID282.html"
The strong produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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249 IENINELIEESKKTIDKNKNATKEEEK-----KKLYQAQY-DLSIYNKQLEEAHNLISVL 302
                                                               362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS, AND CHARACTERIZATION.
MEDLINE=95096166; PubMed=7798308;
Byrd D.A., Swet D.J., Pante N., Cooper C.S., Aebi U., Garace L.;
Saphire A.C.S., Michell P.J., Cooper C.S., Aebi U., Gerace L.;
"Tpr, a large coiled coil protein whose amino terminus is involved in activation of encogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";
J. Cell Biol. 127:1515-1526(1994).
                                                   | : : | | : : | | : : | | EKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIK
                                 -----LLSKKRSLQDERTVIVYVTDTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitchell P.J., Cooper C.S., "The human tpr gene encodes a protein of 2094 amino acids that has extensive coiled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333(1992).
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                               01-0CT-1989 (Rel. 12, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                  2349 AA
                                 EIAKCSEFKPYYLTKALOKLKDLK-
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=93064711; Pubmed=1437155;
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MIM, 189940, -.
GO, GO:0005737; C:cytoplasm; TAS.
                                                                                                 100 ANIOKLIS---ELEEYIK 114
                                                                                                                                 363 FNIDSLFTDPLELEYYLR 380
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16 QVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDL 75
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MOD RES 15
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                                                                                                                                                                                                STRAIN=168;
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                                                                                                                                                                                      FUNCTION
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MEDLINE-98044033; PubMed=9384377;
MEDLINE-98044033; PubMed=9384377;
MEDLINE-98044033; PubMed=9384377;
MEDLINE-980404033; PubMed=9384377;
MEDLINE-980404035; Messieres P., Bolotin A., Borchert S., Barewood V., Bernert S., Berner S., Berner S., Bruschi C.V., Caldwell B., Capuano V., Carrer N.M., Medline S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Benian S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dueschoft A., Ehrlich S.D., Emmerson P.T., Meniac C., Fujita M., Fabret C., Ferrari B., Foulger D., Goffen A., Galiszi A., Galleron N., Anibert H., Holsappel S., Hasch J., Harwood C.R., Haneut A., Albert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Riaerr-Blanchard M., Klein C., Robaysahi Y., Koetter P., Koningstein G., Kroph S., Kumano M., Arita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Redina N., Mellado R.P., Liu H., Moestl D., Nakai S., Noback M.,
                                                                                                                                                                                                                                                                                                                                                                1468 EQHVSVQEMQELKETLNQAETKSKSL------ESQVENLQKTLSEKETEARN 1513
                                                                                                                                                                                                                                                                                                                                                  PYYLT-KALQKLKDL--KLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devine K.M.; "Sequence of the Bacillus subtilis genome between xlyA and ykoR."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                        DB 1; Length 2349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Organic hydroperoxide resistance transcriptional regulator.
                                            COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
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POLY-SER.
POLY-GLU.
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POLY-SER.
MW; AFDD6885CEDCA9EF CRC64;
                                                                                                                                                                                                                                                                              37; Indels
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                        coil; Proto-oncogene; Chromosomal translocation;
 GO:0005643; C:nuclear pore; TAS.
GO:0006606; P:protein-nucleus import; TAS.
                                                                                                                                                                                                                                                                              27; Mismatches
                                                                                                                                                                                                                                                       Score 81.5;
Pred. No. 72
                                                                                                                                                                                                                                  2349 AA; 265600 MW;
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                                                                                                                                                                                                                                                        14.2%;
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                                                                                                                                                                                                                                                                              28; Conservative
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1064
1166
1241
1304
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530
1836
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GO, GO:0005643, C
GO, GO:0006606, P
Coiled coil, Prot
Nuclear protein,
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Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Presecont T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecont B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha B., Roche B., Rock M., Sadale Y.,
A sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Scanse A., Sero S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi B., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tasaro V., Uchlyama S., Vandenbol M., Vannier P., Vasarotti A.,
Vari A., Wambutt R., Wadler E., Wedler H., Weitzenegger T.,
Minters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikwa H.F., Zumstein E., Yoshikawa H., Danchin A.;
subtilis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- FURN. Oxidation on Cys-15 in response to redox signaling leads to the loss of DNA-binding activity and the inactivation of repressor function. Oxidized OhrR can be further reduced by thiol reductants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYSTEINE SULFENIC ACID (-SOH) (PROBABLE). C->G,S: FULL REPRESSOR ACTIVITY, BUT NO MODULATION BY PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21311737; PubMed=11418552; Fuangthong M., Atichartpongkul S., Mongkolsuk S., Helmann J.D.; Fuangthong M., Atichartpongkul S., Mongkolsuk S., Helmann J.D.; "OhrR is a repressor of OhrA, a key organic hydroperoxide resistance determinant in Bacillus subtilis."; J. Bacteriol. 183:4134-4141(2001).
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-!- FUNCTION: Organic peroxide sensor. Represses the expression operoxide-inducible gene ohrA by cooperative binding to two inverted repeat elements.
-!- ENZYME REGULATION: Inactivated by oxidation of Cys-15 to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and repressor activity restored.
SIMILARITY: BELONGS TO THE MARR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO1117; HTH MARR FAMILY, FALSE NEG.
DNA-binding; Transcription regulation; Repressor; Oxidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.1%; Score 81; DB 1; Length 147; 24.7%; Pred. No. 4.1;
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OXIDATION OF CYS-15, AND MUTAGENESIS OF CYS-15.
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Mismatches 34; Indels

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Matches
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:: | :: | |: | : | :: | : | EMTKQYKPLLDKLITYPQYLAL-LILWEHETLTVKKWGEQLYLDSGTLTPMLKRMEQQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).

-!- MISCELLANDOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=26595 / ATCC 700392;
MEDLINE=971394467; PubMed=9252185;
MEDLINE=971394467; PubMed=9252185;
MEDLINE=971394467; PubMed=9252185;
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Loftus B., Richardson D., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Danas M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Venter J.C.,
                                                                                                                                                                                                                                                                                                                    Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pylori.";
Nature 388:539-547(1997).
-!- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate
-!- Pyruvate + L-glutamate.
-!- PATHWAY: Tryptophan biosynthesis; first step.
-!- SATHWAY: Tryptophan biosynthesis; first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 500;
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InterPro; IPR006801; Anth—synth—chor.
InterPro; IPR005257; TrpE_prot.
Pfam; PF04715; Anth synt I N; I
Pfam; PF04715; Anth synt I N; I
ProDom; PD00079; Antranate bind; I.
PRINTS; PR00995; Antranase bind; I.
TIGRPAMs; TIGR00565; trpE proteo; I.
TIGRPAMs; TIGR00565; trpE proteo; I.
Tryptophan biosynthesis; Lyase; Complete proteome.
SEQUENCE 500 AA; 56556 MW; B28485C36E1E635E CRC64;
                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB--2003 (Rel. 41, Last annotation update)
Anthranilate synthase component I (EC 4.1.3.27)
TRPE OR HF1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
15;
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Pred. No.
                                                                              |:::||| :|||:|:||:
GLITRKRSEEDERSVLISLTE 102
                                                     76 KLLSKKRSLQDERTVIVYVTD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE000632; AAD08326.1; -. PIR, B64680, B64680, B64680, HSSP; P00897; 117Q. TIGR, HP1282; -.
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28.3%;
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Best Local Similarity
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025869;
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                                                                          138 SFEMLNFFEDLPHLKAKDNTVHDF1FYLAQNLIIIDHKEKSVEILGAC--FDERFKTEIA 195
                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLETE GENOME.
STRAIN=India-1967 / Isolate Ind3;
MEDLINE=33202281, PubMed=8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variala and vaccinia viruses necessary to overcome the host Paris mechanisms.";
FESS Lett. 319:80-83(1993).
                                      14 TFQVKKFFRD---TKKKFNLNYEEI-YILNHILRSESNEISSKEIAKCSEFKPYYLTKAL
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                 70 OKLKDLKLLSK-----KRSLQDERTVIVYVTDTQKANIQKLISELEEYIK 114
                                                                                                                                     OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Potential virulence determinants in terminal regions of variola smallpox virus genome.";
Nature 366:748-751(1993).
  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=India-1967 / Isolate Ind3;
MEDLINE=93190624; PubMed=838392;
Shchelkunov S.N., Blinov V.M., Totmenin A.V., Marennikova S.S.,
Kolykhalov A.A., Frolov I.V., Chizhikov V.E., Gytorov V.V.,
Gashikov P.V., Belanov B.F., Belavin P.A., Resenchuk S.M.,
Andzhaparidze O.G., Sandakhchiev L.S.;
"Nucleotide sequence analysis of variola virus HindIII M, L, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: This enzyme consists of at least eight subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bangladesh-1975;
MEDLINE=84086747; PubMed=8264798;
Massung R.E., Esposito J.J., Liu L., Qi J., Utterback T.R.,
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
                                                                                                                                                                                                                                                                                   01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
DNA-directed RNA polymerase 147 kDa polypeptide (EC 2.7.7.6).
RPO147 OR LGR OR JGR.
  Indels
39;
  24; Mismatches
                                                                                                                                                                                                                                                   PRT; 1286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, X67119, CAA47582.1; -.
EMBL, S55844, AAB24679.1; -.
EMBL, X65198; CAA49024.1; -.
EMBL, L22579; AAA60831.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virus Res. 27:25-35(1993).
  32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=10255;
                                                                                                                                                                                                                                                                                                                                                                                    Variola virus.
                                                                                                                                                                                                                                                                                                                                                                                                                         Orthopoxvirus
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VARV
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33 EEIYILNHI-----LRSE---SNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLSKKRS 83
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14.1%; Score 81; DB 1; Length 1286;
Best Local Similarity 30.8%; Pred. No. 42;
Matches 33; Conservative 16; Mismatches 20; Indels 38; Gaps
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                                  PIR, T18521; T28521.
InterPro; IPR00722; RNA_pol_A.
InterPro; IPR007083; RNA_pol_Rbbl_4.
InterPro; IPR007083; RNA_pol_Rbbl_4.
InterPro; IPR007081; RNA_pol_Rbbl_4.
InterPro; IPR007081; RNA_pol_Rbbl_5.
InterPro; IPR00522; RNA_pol_Rbbl_5.
InterPro; IPR00653; RNA_pol_Rbbl_7.
InterPro; IPR00653; RNA_pol_Rbbl_7.
InterPro; IPR00653; RNA_pol_Rbbl_7.
InterPro; IPR00663; RNA_pol_Rbbl_7.
InterPro; IPR00663; RNA_pol_Rbbl_7.
INTERPRO; INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPROINA, INTERPRO
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SEQUENCE 1286 AA; 146782 MW; EE9965ACBIDFA93B CRC64;
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Search completed: November 17, 2003, 12:43:37 Job time : 18 secs

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SarR (Staphylococal accessory regulator A homolog) SARR (Staphylococal accessory regulator A homolog) SARR (SA7295 OR SA2089 OR MW213.
Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), Atchylococcus aureus (strain MW2).
Staphylococcus aureus (strain MW2).
Batteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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01-MAR-2001
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1 MSKINDINDLVNATFQVKKF......DTQKANIQKLISELEEYIKN 115
                                                                                                                                                                                                                                         830525
, GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                         November 17, 2003, 12:24:25
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Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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sp_phage:*
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sp_rodent:*
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sp_vorters:*
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sp_bacteriap:*
sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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length: 2000000000
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sp_bacteria:*
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sp_human:*
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Maximum DB seq
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                                                                                                                           Title:
Perfect :
                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9f0rl staphylococ	Q8cnc4 staphylococ	Q53600 staphylococ	053777 staphylococ	085233 staphylococ	Q99ta4 staphylococ	Q9ezk4 staphylococ	Q99rd5 staphylococ	Oscnu6 staphylococ	Q9rfj6 staphylococ	Q9kwj2 staphylococ	Q8i3p4 plasmodium	Q96xy0 sulfolobus	Q99s05 staphylococ	Q8pgp1 xanthomonas	OScres stanhylogod
ΩI	Q9F0R1	Q8CNC4	053600	053777	085233	Q99TA4	Q9EZK4	Q99RD5	QBCNU6	Q9RFJ6	Q9KWJ2	Q8I3P4	0AX36Ö	508660	Q8PQP1	OSCRES
	191	16	16	0	16	16	(7	16	16	N	16	ro			16	
% Query Match Length DB	115	114	124	113	124	153	247	247	66	166	250	1777	131	116	153	242
% Query Match	100.0	84.7	25.8	25.4	24.9	21.4	21.4	21.4	20.9	20.9	20.0	18.4	18.0	17.7	17.6	17.3
Score	574	486	148	146	143	123	123	123	120	120	115	105.5	103.5	101.5	101	99.
Result No.	-	7	٣	4	ιν	9	7	œ	σv	10	11	12	13	14	15	16

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=MUSO. and N315,
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba J.
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus

Lancet 357:1225-1240(2001).

SEQUENCE FROM N.A.

STRAIN=RN6390; Cheung A.L., Manna A.C.; "Characterization of sark, a modulator of sar expression in Staphylococcus aureus."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

[1] SEQUENCE FROM N.A.

Q93r11 xanthomonas	Q8xlt0 clostridium		Q8cq27 staphylococ		Н	~~		Q8eyb8 leptospira		Q8nv85 staphylococ	Q8i386 plasmodium	08xjp0 clostridium		. Q8pds2 xanthomonas	Q8i3z6 plasmodium	P70734 acinetobact	050574 bacillus ps	Q92qq1 rhizobium m	Q8d349 wiggleswort	O51465 borrelia bu	Q8ifm4 plasmodium	Q8mwp2 plasmodium	Q8mwpl plasmodium	Q8mwh2 plasmodium	Q8crf1 staphylococ	32 1	a0 f	so.
Q93R11								Q8EYB8			Q8I386		Q814T0		981326	P70734	050574				Q8IFM4	Q8MWP2	QSMWP1	Q8MWH2			QBR6A0	054123
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## ALIGNMENTS

115 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 12228;
STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016750; AA005509.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 22, Last amnotation update)
Staphylococcal accessory regulator variant (Staphylococcal accessory
                                                                                                                                                                                                                                                 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Baba T., Taweuchi F., Kuroda M., Yuzawa H., Kuroda H.,
Vandani Y., Inama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatau K.,
"Genome and virulence determinants of high virulence community-
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                                                                                                                                                         100.0%; Score 574; DB 16; Length 115; 100.0%; Pred. No. 1.5e-36; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
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Pred. No. 6.9e-30;
8; Mismatches 10; Indels
                                                                                                                                   115 AA; 13669 MW; D2CE40E2DB234DBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 114 AA; 13590 MW; A401B6F9FE6BBCAB CRC64;
                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                              PRT;
                                                      acquired MRSA.";
Lancet 359:1819:1827(2002).
EMBL, AP0207701; AAG35715:1; -.
EMBL, AP00334; BAB58457.1; -.
EMBL, AP003136; BAB943387.1; -.
EMBL, AP004829; BAB96078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.7%;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis
                                                                                                                                                                     Best Local Similarity 100.0
Matches 115; Conservative
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es 96; Conservative
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SEQUENCE 115 AA;
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MEDLINE-92335318; PubMed=1321441;
Cheung A.L., Koomey J.M., Butler C.A., Projan S.J., Fischetti V.A.;
"Regulation of exoprotein expression in Staphylococcus aureus by a
locus (aar) distinct from agr.";
Proc. Natl. Acad. Sci. U.S.A. 89:6462-6466(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES_S.aureus; STRAIN=MUSO, and N315;
MEDLINE=21311952; PubMed=11410146;
Kurdda M. Ohta T. Uchlyama I. Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Katanaori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani UI. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekintzu K., Hirakava H., Kuhara S., Goto S., Yabuzaki J.,
Sekintzu K., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba 'Hattori M., Qasawara N., Harabashi H., Hiramatsu K.; Furuya K., Yoshino C., Shiba 'Mhole genome sequencing of meticillin-resistant Staphylococcus
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SEQUENCE FROM N.A.
SEQUENCE S. aureus; STRAIN=WWZ;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Tamamouch K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-acquired MRSA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheung A.L., Projan S.J.; "Cloning and sequencing of sarA of Staphylococcus aureus, a gene "Cloning and sequencing of sar."; required for the expression of agr."; Jacteriol. 176:468-4172(1994).
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                                                                                                                                                                                                                                                       SPECIES=S.aureus;
Shawcross S.G., Edwards-Jones V., Dawson M.M., Foster H.A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheung A.L.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
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Staphylococcus aureus (strain Muso / ATCC 700699), Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2). Bacteria, Firmicutes; Bacillales; Staphylococcus.
                              Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2).

Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280, 158878, 158879, 196620;
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SPECIES-S.aureus; STRAIN=RN450;
MEDLINE-94292439; PubMed-8021198;
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SPECIES=S.aureus; STRAIN=RN450;
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regulator A). SARA OR SAVO616 OR SA0573 OR MW0580. Staphylococcus aureus,

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14731 MW; 4D1D10E47D574266 CRC64;
                     24.9%; Score 143; DB 16; 1
29.2%; Pred. No. 0.00076;
tive 25; Mismatches 55;
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(TrEMBLrel. 17, Last seg
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EMBL; AP003363; BAB57926.1; -.
EMBL; AP003135; BAB42851.1; -.
CMBL; AP0048028; BAB95570.1; -.
COMDICTE PROCESSES.
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
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                                              33; Conservative
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124 AA;
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STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fluckiger U., Wolz C., Cheung A.L.; "Characterization of a sar homolog of Staphylococcus epidermidis."; Infect. Immun. 0:0-0(1998).
KQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRI 115
                                                                                                                                                                                                                                                                                                          Cheung A.L., Projan S.J.;
"Cloning and sequencing of sarA of Staphylococcus aureus, a gene required for the expression of agr.";
Bacteriol. 176:416249.
EMBL: U46541; AAB05396.1; -.
SEQUENCE 113 AA; 13469 MW; 6A6D53F34E010AFB CRC64;
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Last annotation update)
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                      Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
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MEDLINE=94292439; PubMed=8021198;
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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SERAIN=Mus0, and N315;

MEDLINE=21311951; PubMed=11418146;

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Muzakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hizakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furnya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."] 1 MSKINDINDLVNATFQ-----VKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKE 21 MKKVN--NDTVFGILQLETLLGDINSIFSEESKYKMSREEILLL--LTLWQKGSMTLKE 3 ISKINDCFELLAMVTYADRLKGIIKKEFSISFEEFAVLTYISENKEESYYLKDIINHLNY 14; Gaps Gaps MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Magai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-.; 0 61 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI Length 153; Indels Indels 153 AA; 18009 MW; E24C6E9BCC353F20 CRC64; Last sequence update) Last annotation update) Repressor of toxins Rot.
ROT OR SAV1764 OR SA1583 OR MW1705.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain M315), and
Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI\_TaxID=158878, 158879, 196620; 45; 21.4%; Score 123; DB 16; ilarity 28.0%; Pred. No. 0.03; Conservative 26; Mismatches 45;

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EMBL, AP003137; BAB43590.1; -. EMBL, AP048830. BAB96283.1; -. Complete proteome. SEQUENCE 247 AA; 29793 MW;
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SEQUENCE FROM N.A.
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01-MAY-2000 (
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Q8CNU6;
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.,
"Genome and virulence determinants of high virulence community-
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01-UTN-2001 (TYEMBLEEL: 17, Last sequence update)
01-OCT-2002 (TYEMBLEEL: 22, Last annotation update)
SARH2 protein (Steaphylococcal accessory regulator A homolog).
SARH2 OR SAV2499 OR SA2287 OR MW2418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%; Score 123; DB 2; Length 247; 27.8%; Pred. No. 0.048; ive 26; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288788; AAG45334.2; --
SEQUENCE 247 AA; 29792 MW; D078366866F60B2B CRC64;
                                                                                                                                                         Last sequence update)
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Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain MW2).
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1280;
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Lancet 359:1819-1827(2002).
EMBL; AP003365; BAB58661.1; -.
                                                                                                         01-MAR 2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
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                                    PRELIMINARY;
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                                        Q9EZK4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 LNYEETYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERT
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Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE016748; AA005034.1; -.
Complete proteome.
SEQUENCE 99 AA; 11800 MW; 588D68BC9BF837AE CRC64;
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                                                       Length 247;
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                                              21.4%; Score 123; DB 16; Length 2 27.8%; Pred. No. 0.048; Ative 26; Mismatches 52; Indels
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247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
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EMBL, AB033454; BAB03341.1;
EMBL, AP001129; BAB41327.1;
EMBL, AB050858; BAB69826.1;
EMBL, AP00338; BAB56274.1;
EMBL, AP004822; BAB93950.1;
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SEQUENCE 1777 AA;
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Best Local Similarity
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SEQUENCE 250 AA;
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                                                                                                                                                               90 MDRFVEVKYRTKTYNNLVELEWIYKERPVDDERTVIIHFNEKLOOEKVELNFISD 147
                                                                                                                 34 MKKVN--NDTVFGILQLETLLGDINSIFSEIESEYKMGREEILIL--LTLMQKGFMTLKE
                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINENSIS, and Muso / ATCC 700699;
MEDLIKE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizurani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kahehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Soshino C., Shiba
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kuroda M., Kuwahara-Arai K., Hiramatsu K.;
Identification of the up- and down-regulated genes in vancomycin-
resistant Staphylococcus aureus strains Mu3 and Mu50 by cDNA
differential hybridization method.";
                                                                                                                                                                                                                                                        MEDLINE=22040717; PubMed=12044378; MEDLINE=22040717; PubMed=12044378; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi Magai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamanoto K., Hiramatus K.; "Genome and virulence determinants of high virulence community-
                                                                          14;
                                                   Length 166;
J. Bacteriol. 182:3197-3203(2000).
EMBL, AF189239; AAF22306.1; -.
SEQUENCE 166 AA; 19431 MW; 251AE45481E5699D CRC64;
                                                20.9%; Score 120; DB 2; Le
28.0%; Pred. No. 0.055;
ive 26; Mismatches 45;
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                                                          Local Similarity 28.09
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MEDLINE=2255708; PubMed=12368867;
Mall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Cheristodoulou Z., Clark L., Clark R., Corton C., Croin A., Davis B., Dear P., Dearden F., Doggett J., Croin B., Goodhead I., Gable M., Goodhead I., Gailliam R., Hamlin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Harper D., Hancer H., James K.D., Johnson D., Lennard N., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., McJean J., Mooney P., Moule S., Murphy L., Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E., Asjandrem M.A., Rutter S., Kutherford K.M., Sanders M., Simmonds M., Seeger K., Sharp S., Smith R., Squares S., Stevens K., Aulston J. E., Craig A., Nawhold C., Barrell B.G., Sulston J. E., Craig A., Nawhold C., Barrell B.G., Stevens M., Stephen C., Craig A., Nawhold C., Barrell B.G., Stevens M., Stephen C., Elar M., Mallston J. E., Craig A., Nawhold C., Barrell B.G., Stevens M., Stephen C., Elar M., Sanders M., Stephen C., Elar M., Stephen C., Elar M., Sander M., Sander M., Stephen C., Craig A., Nawhold C., Barrell B.G., Stevens M., Stephen C., Elar M., Sander M., Stephen C., Craig A., Nawhold C., Barrell B.G., Stevens M., Stephen C., Elar M., Sander M., Stephen C., Stephen
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                                                                                                                                                                                                                                                                           6 DINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYL
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Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                       DB 16; Length 250;
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4680D50FE86DDC19 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                              55;
                                                                             20.0%; Score 115; DB 1
25.0%; Pred. No. 0.19;
ive 26; Mismatches
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250 AA; 29890 MW;
                             Query Match
Best Local Similarity 25...
- hes 27; Conservative 2
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EMBL; AL929353; CAD51583.1;
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host specificities.";
Nature 417:459-463(2002).
EMBL; AE011653; AAM35173.1; -.
Interpro; IPR000835; HTH Mark.
Pfam; PF01047; Mark; 1.
PRINTS; PR00598; HTHMARR.
                                                                           Lancet 357:1225-1240(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Conservative
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                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                STRAIN=MW2
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Q8PQP1;
                                                       aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
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                                                                                                                                                                                                                                                                                                                          Archaea, Crenarchaeota, Thermoprotei, Sulfolobales, Sulfolobaceae, Sulfolobus.
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01-JUN 2001 (TrEMBLrel. 17, Last sequence update)
01-JUN 2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SAV2267 (Hypothetical protein MW2185).
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain Mu2), and
Staphylococcus aureus (strain MW2).
Bacteria: Firmicutes; Bacillales; Staphylococcus.
NCBL TAXID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of an aerobic thermoacidophilic Cenarchaeon, Sulfolobus tokodaii strain?";

DNA Res. 8:123-140(2001).

EMBL; AP000989; BAB67497.1; -.

InterPro.; IPR000895; HTH MarR.

PRINTS; PR00598; HTHMARR.

PRINTS; PR00598; HTHMARR.

SMART; SM0047; HTH MARR.

Hypothetical protein; Complete proteome.

SEQUENCE 131 AA; 15129 MW; E0A0AB5A3521EG3B CRC64;
                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein ST2388.
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                                                                                                           PRELIMINARY;
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STRAIN=JCM 10545 / 7;
Pubmed=11572479;
                                                                                                                                                                                                                                                                                                      Sulfolobus tokodaii
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DD 099805;
DT 099805;
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REDLINE=22022145; PubMed=12024217;

REDLINE=22022145; PubMed=12024217;

REDLINE=22022145; PubMed=12024217;

REDLINE=22022145; PubMed=12024217;

REDLINE=22022145; PubMed=12024217;

RESTOR N.A., Reinach F.C., Farran C.B., Alweida N.F., Quaggio R.B., Alweida N.F., Cardazo J., Chambergo F., Ciapina L.P., Faria J.B., Forneidhieri B.F., Franco M.C., Curiano-Santos J.R., Ferrei B.P., Franco M.C., Grebon S.G.M. N.F., Fornighieri B.C., Machado M.C., Grebon B.G.M., Martine E.C., Maidadnis J.M. Madeira A.M., Martine E.C., Maidadnis J.M. Menck C.P.M., Mayaki C.Y., Moon D.H., Movelira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Tarkten M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D., Spinola L.A.F., Tarkten M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D., Studal J.C., Kitajima J.P., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., Traffi D., Tsai S.M., White F.F., Trongens with differing M.F. Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Strander Stran
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Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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EMBL, AP003364; BAB58429.1; -.

EMBL, AP0048136; BAB4359.1; -.

EMBL, AP004829. BAB96050.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 116 AA; 13986 MW; CE7ACED821E33EF9 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SQ SEQUENCE 153 AA; 16888 MW; 58C5D2CE5B3C71AA CRC64;
Query Match
Best Local Similarity 29.7%; Pred. No. 1.4;
Matches 27; Conservative 22; Mismatches 40; Indels 2; Gaps 1;
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Search completed: November 17, 2003, 12:44:37 Job time : 56 secs

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Title: Perfect score:

Seguence:

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Run on:

Scoring table:

Searched:

Database :

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JAPAICANT: Trustees of Dartmouth College
TITE OF INVENTION: Compositions and Methods for affecting virulence determinants in TITE OF INVENTION: Dacteria
FILE REPERENCE: 11312-006-228
CURRENT APPLICATION WHERE: PCT/US02/00877
CURRENT APPLICATION WHERE: PCT/US02/00877
CURRENT FILING DATE: 2003-03-04
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
LENGTH: 115
TYPE: RT
CORRANISM: Staphylococcus aureus
PCT-US02-00877-2
                                                                                                                                                                                                                                                     Sequence 35, Appl Sequence 35, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 5, Appl Sequence 5151, Ap Sequence 5151, Ap Sequence 7381, Ap Sequence 6116, Appl Sequence 7218, Appl Sequence 7218, Appl Sequence 7218, Appl Sequence 28, Appl Sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Appl
Sequence 28, Appl
Sequence 6537, Ap
Sequence 6537, Ap
Sequence 6537, Ap
Sequence 5857, Ap
Sequence 5857, Ap
Sequence 6519, Ap
Sequence 6519, Ap
  Sequence 2, Appli
Sequence 48, Appli
Sequence 6523, Ap
Sequence 6523, Ap
Sequence 6523, Ap
Sequence 6487, Ap
Sequence 26, Appl
Sequence 26, Appl
6 US-10-043-539-2

CUS-08-353-2

US-08-353-2

US-08-353-4-2

US-08-35-11-529-6523

EUS-08-20-11-529-6523

EUS-08-20-11-529-6523

EUS-10-043-539-26

EUS-10-043-539-35

EUS-10-043-539-3

EUS-10-095-111A-5614

EUS-10-095-111A-5614

EUS-10-095-111A-5614

EUS-10-095-111A-5614

EUS-10-095-111A-5614

EUS-10-043-539-28

EUS-10-043-539-28

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EUS-10-043-539-28

EUS-10-043-539-28

EUS-10-043-539-5857

EUS-10-08-827-356-4158

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     RESULT 1
PCT-US02-00877-2
                                                                                                                                                                                    Sequence 2, Appli
                                                                                                                                                                       November 17, 2003, 12:43:21; Search time 159 Seconds (without alignments) 658.117 Million cell updates/sec
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574
1 MSKINDINDLVNATFQVKKF......DTQKANIQKLISELBEYIKN 115
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1: /cgtl2 6/ptodata/2/paa/USG6 COMB.pep:*
2: /cgtl2 6/ptodata/2/paa/USG6 COMB.pep:*
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19: /cgtl2 6/ptodata/2/paa/USG9 COMB.pep:*
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- 2003 Compugen Ltd.
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                                                                                                                              sw model
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Gapop 10.0 , Gapext 0.5
                             GenCore (c) 1993
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Maximum Match 100%
                                                                                                                            protein search, using
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Maximum DB seq length: 2000000000
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Match Length DB
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574

Score

Result No.

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1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Raten J. Shaw
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS RELATED
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 5574
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering S.
                                                                                                                     Query Match 100.0%; Score 574; DB 26; Best Local Similarity 100.0%; Pred. No. 3.6e-49; Matches 115; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match-
100.0%; Score 574; DB 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 115; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schering-Plough Corporation 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PARCENTIN
SOFTWARE: PARCENTIN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,356
FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,477
FILING DATE: 01-APR-1996
APPLICATION NUMBER: 60/016,743
FILING DATE: 02-MAY-1996
APPLICATION NUMBER: 60/020,016
FILING DATE: 14-UN-1996
INFORMATION FOR SEQ ID NO: 4882:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4882, Application US/08827356
GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
                                ORGANISM: Staphylococcus aureus
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1...129
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                                                              US-10-043-539A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2 Application US/10043539;
GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Manna, Adar
APPLICANT: Manna, Adar
TITLE OF INVENTION: BACTERIA
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: DC-0199
CURRENT APPLICATION NUMBER: US/10/043,539
CURRENT APPLICATION NUMBER: US/202-01-11
FILE REPERENCE: DC-0199
CURRENT FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR PLILING DATE: 2001-01-12
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Sequence 2, Application US/10043539A

Sequence 2, Application US/10043539A

Sequence 2, Application US/10043539A

Sequence 2, Application US/10043539A

Sequence 3, Application Ambrose

APPLICANT: Cheung, Ambrose

APPLICANT: Manna, Adar

APPLICANT: Common Adar

FILE REFERENCE: DC-0199

CURRENT FILING DATE: 2000-01-11

PRIOR PILING DATE: 2001-01-12

PRIOR PILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 35

SEQ ID NOS: 35

LENGTH: 115
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                                                                                                                            1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
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                                                                    Gaps
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      Length 115
                                                                 0; Indels
100.0%; Score 574; DB 1;
100.0%; Pred. No. 3.6e-49;
tive 0; Mismatches. 0;
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; ORGANISM: Staphylococcus aureus
US-10-043-539-2
                                                              Matches 115; Conservative
      Query Match
Best Local Similarity
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APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-09A
CURRENT APPLICATION NUMBER: US/09/450,969
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 7544
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: George H. Miller
APPLICANT: George H. Miller
APPLICANT: George H. Miller
APPLICANT: George H. Miller
APPLICANT: Raren J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
CURRENT APPLICATION NUMBER: US/09/950,084
CURRENT FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR APPLICATION NUMBER: US 09/266,542
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          1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
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                                                                     MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
                                                                                                                                                                               Gaps
                                                                                                                                              61 KPYYLTKALOKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN 115
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100.0%; Score 574; DB 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 115; Conservative 0; Mismatches 0;
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CRGANISM: Staphylococcus aureus
US-09-950-084-6523
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LENGTH: 129
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Sequence 6223, Application Us/05611529

SEQUENCE 6223, Application Us/05611529

SEQUENCE 6223, Application Us/05611529

SEQUENCE 6223, Application Us/05611529

PROPERTY George H. Siliar T.

SECUENCE CONTRIBUTION NUMBER: US/09/611,529

CURRENT FILING DATE: 2000-66-30/913,718

PROB PRICHARD DATE: 1999-07-14

PROB PRICHARD DATE: 1999-07-14

PROB PRICHARD DATE: 1999-07-14

PROB PRICHARD DATE: 1999-07-14

PROB PRICHARD DATE: 1999-03-10

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Pred. No. 4.2e-49;
; Mismatches 0;
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Best Local Similarity 100.
Matches 115; Conservative
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SEQ ID NO 6523
                                                                                                                                       RESULT 5
US-09-611-529-6523
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ORGANISM:
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Gaps

62

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Sequence 26, Application US/10043539
GENERAL INFORMATION:
APPLICANT: Chang, Ambrose
APPLICANT: Chang, Ambrose
APPLICANT: Chang, Adar
APPLICANT: Zhang, Adar
APPLICANT: Zhang, Androse
APPLICANT: Zhang, Androse
APPLICANT: Anna, Adar
APPLICANT: Anna, Adar
APPLICANT: Anna, Adar
APPLICANT: Anna, Adar
APPLICANT: Anna, Adar
APPLICANT: Anna, Adar
APPLICANT: Chang, Gongyi
TITLE OF INVENTION: Changes: US/10/043,539
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-05-08
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE

LOCATION: 2,4,10,15,16,17,19,20,24,25,31,38,44,45,47,51,52,58,59,61,73,77,78,86,

LOCATION: 87,95,97,99,102, 106,110,114,117,118,120

CTHER INFORMATION: Xaa = any amino acid

PCT-US02-00877-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYBBIYILNHILRSBSNBISSKBIAKCSBF 60
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                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch
1 Similarity 43.9%; Score 224; DB 1; Length 120;
50; Conservative 15; Mismatches 49; Indels
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LOCATION: (19)...(20
LOCATION: (19)...(30
FEATURE INFORMATION: "X" is defined as any amino acid residue.
FEATURE:
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LOCATION: (2)..[(2)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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OTHER INFORMATION: "X" is defined as any amino acid
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OTHER INFORMATION: "X" is defined as any
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SEQ ID NO 26
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
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NAME/KEY: MISC FEATURE
LOCATION: (15)..(17)
OTHER INFORMATION: "X"
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NAME/KEY: MISC_FEATURE
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                          Score 486; DB 18;
Pred. No. 2.7e-40;
8; Mismatches 10;
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Pred. No. 2.7e-40;
8; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.7%;
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.2%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.2<sup>3</sup>
Matches 96; Conservative
                                                                                             TYPE: PRT
) ORGANISM: S.epidermidis
US-09-450-969-6487
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US-10-092-411A-4993
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PCT-US02-00877-26
         SEQ ID NO 6487
LENGIH: 128
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us-10-043-539a-2.rapm

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NAME/KEY: MISC FEATURE
LOCATION: (31)..(31)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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INFORMATION: "X" is defined as any amino acid residue.
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COCATION: (114).
CHER. INFORMATION: "X" is defined as any amino acid residue.
FEATURE:
                      LOCATION: (24)...(25)
DTHER INFORMATION: "X" is defined as any amino acid residue
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LOCATION: (44)...(45)
OTHER INFORMATION: "X" is defined as any amino acid residue
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LOCATION: (95)...(95)
DIHER INFORMATION: "X" is defined as any amino acid residue.
                                                                                                                                                                                                                                             LOCATION: (38)...(38)
OTHER INFORMATION: "X" is defined as any amino acid residue
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INFORMATION: "X" is defined as any amino acid residue
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INFORMATION: "X" is defined as any amino acid residue
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"THER INFORMATION: "X" is defined as any amino acid residue
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R INFORMATION: "X" is defined as any amino acid residue
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IER INFORMATION: "X" is defined as any amino acid residue
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THER INFORMATION: "X" is defined as any amino acid residue
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OTHER INFORMATION: "X"
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OTHER INFORMATION: "X"
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NAME/KEY: MISC_FEATURE
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APPLICANT: Cheung, Ambrose
APPLICANT: Manna, Adar
APPLICANT: Cheung, Gongyi
ITTLE CART. Zhang, Gongyi
ITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
FILE REFERENCE: DC-0199
CURRENT APPLICATION NUMBER: US/10/043,539A
CURRENT FILING DATE: 2000-01-11
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 120
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                                                                                                                                                                                                                                                                                                                                                       62
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39.0%; Score 224; DB 26; Length 120;
Best Local Similarity 43.9%; Pred. No. 4.2e-14;
Matches 50; Conservative 15; Mismatches 49; Indels
                                             FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (120)

COTHER INFORMATION: "X" is defined as any amino acid residue.
US-10-043-539-26
LOCATION: (117)..(118)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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DTHER INFORMATION: "X" is defined as any amino acid residue.
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OTHER INFORMATION: "X" is defined as any amino acid residue.
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OTHER INFORMATION: "X" is defined as any amino acid residue.
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OTHER INFORMATION: "X" is defined as any amino acid residue
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OTHER INFORMATION: "X" is defined as any
FEATURE:
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NAME/KEY: MISC FEATURE
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NAME/KEY: MISC_FEATURE
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PCT-US02-00877-35

FCT-US02-00877-35

Sequence 35, Application PC/TUS0200877

SEQUENCE 35, Application PC/TUS0200877

SEQUENCE 35, Application PC/TUS0200877

SEQUENCE INVENTION: Compositions and Methods for affecting virulence determinants in TITLE OF INVENTION: Deacteria

TITLE OF INVENTION: Deacteria

FILE REFERENCE: 11312-006-228

CURRENT APPLICATION NUMBER: 9C7/US02/00877

CURRENT FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-01-01

PRIOR FILING DATE: 2001-03-08

SOFTWARE: PATENTION NUMBER: 60/289,601

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39.0%; Score 224; DB 26; Length 120; 43.9%; Pred. No. 4.2e-14; tive 15; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureus
   Query Match
Best Local Similarity 43.9%
Matches 50; Conservative
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                                                                                                                                                     Gaps
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                                                                                                       Length 124;
                                                                                                                                                     52; Indels
                                                                                                  Query Match 25.8%; Score 148; DB 20; Best Local Similarity 30.1%; Pred. No. 1.8e-06; Matches 34; Conservative 27; Mismatches 52;
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he : 161 secs
                , ORGANISM: Staphylococcus aureus US-09-612-549A-1
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Job time
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; Sequence 1, Application US/09612549A
; General Invormation:
APPLICANT: HURLBURT, Barry
APPLICANT: HURLBURT, Barry
; APPLICANT: WHILL BARRY
TITLE OF INVENTION: LAPPLICACCCAL VIRULENCE PACTORS AND THE USE THERE
TITLE OF INVENTION: STAPHYLOCOCCAL UNFECTIONS
TITLE OF INVENTION: STAPHYLOCOCCAL UNFECTIONS
TITLE OF INVENTION: STAPHYLOCOCCAL INFECTIONS
TOURENT APPLICATION NUMBER: US/09/612,549A
CURRENT FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENT VERSION 3.0
SEQ ID NO 1
LENGTH: 124
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for affecting virulence determinants in TITLE OF INVENTION: Dacteria
FILE REFERENCE: 11312-06-228
CURRENT APPLICATION NUMBER: PCT/US02/00877
CURRENT PILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261,533
PRIOR PILING DATE: 2001-01-12
PRIOR PILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-03-04
NUMBER: 60/263,601
PRIOR FILING DATE: 2001-03-04
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
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                                                                                                       Length 120;
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                                                                                                                                                        52; Indels
                                                                                                  Query Match

25.8%; Score 148; DB 26;
Best Local Similarity 30.1%; Pred. No. 1.7e-06;
Matches 34; Conservative 27; Mismatches 52;
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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-043-539A-35
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Matches 34; Conservative
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PCT-US02-00877-3
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US-10-469-477-2

Sequence 2, Application US/10469477

GENERAL INFORMATION:

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GENERAL INFORMATION:

COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN 1

FILE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN 1

FILE REPEREBNUE: DC-0188

CURRENT APPLICATION NUMBER: US 60/273, 791

PRIOR APPLICATION NUMBER: US 60/273, 791

PRIOR PELLOR DATE: 2001-08-15

PRIOR PELLOR DATE: 2001-08-15

PRIOR FILING DATE: 2001-08-15
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Sequence 25, Appl
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2207,                                                                                                                                                     ; Search time 68 Seconds
(without alignments)
82.045 Million cell updates/sec
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574
1 MSKINDINDLVNATFQVKKF......DTQKANIQKLISELEEYIKN 115
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(Ggn2_6/ptodata/2/paa/US00_NEW_COMB.pep:*):

(Ggn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*):

(Ggn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*):

(Ggn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*):

(Ggn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*):

(Ggn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*):

(Ggn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*):
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-10-425-114A-68716
US-10-332-089-2
US-10-679-063-25933
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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No.
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APPLICANT: Trustees of Dartmouth College
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN BA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN BA
TITLE REPERBNEE: DC-0.18
CURRENT APPLICATION NUMBER: US 60/273,791
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-08-15
PRIOR PILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATCHTIN NUMBER: US 60/329,140
PRIOR PILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 4
LENGTH: 134
TYPE: PRT
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                                     719, App
26949, A
801, App
25945, A
55228, A
2544, App
2, Appl
16, Appl
16, Appl
16, Appl
25946, A
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US-09-976-88-251

US-10-473-040-719

US-10-473-040-719

US-10-679-663-26949

US-10-296-115-81

US-10-679-663-25945

US-10-679-663-25945

US-10-679-663-25983

US-10-679-063-25983

US-10-205-516A-16

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US-10-205-516A-16
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US-10-679-063-25939
US-10-679-063-25940
US-10-679-063-25941
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Best Local Similarity 28.4%; Pred. No. 8.8;
Matches 25; Conservative 25; Mismatches 35;
                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOKLKDLKLLSKKRSLQDERTVIVYVTD 96
                                                                                                                                                                                                                                                Sequence 4, Application US/10469477 GENERAL INFORMATION:
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US-10-469-477-4
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21; Gaps

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APPLICANT: Yurieve, Olga
APPLICANT: Yurieve, Olga
APPLICANT: Yurieve, Olga
APPLICANT: Yurieve, Olga
APPLICANT: Jeruzalmi, David
APPLICANT: Burck, Inina
APPLICANT: Burck, Inina
APPLICANT: Wirina
APPLICANT: Wiriyan, John
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
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TITLE OF INVENTION: UNMBER: US/09/716,964A
FRIOR FILING DATE: 1907-04-08
FRIOR PELING DATE: 1997-04-08
FRIOR PELING DATE: 1997-04-08
FRIOR FILING DATE: 1997-04-08
FRIOR FILING DATE: 1997-04-08
FRIOR FILING DATE: 1998-04-08
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 25
LENGTH: 260
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                                                                                                                                                              99 SKLGHVTSLSNVE---KEFILDIPNKPKTLTTEEPPVFPKTLVLNEQHATEETSLMRKTL 155
                                                                                                                                                                                                                                     55 AKCSEFKPYYLIK----ALQKLKDLK-----LLSKKRSLQDERTVIVYVTDTQKANIQK 104
                                                                                                  2 SKINDINDLVNATFQVKKFFRD-TKKKFNLNYEE-----IYILNHILRSESNEISSKEI 54
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                                      51; Indels
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24.2%; Pred. No. 65; tive 28; Mismatches
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14.2%; Score 81.5; D
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches
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US-10-673-119-25
Sequence 25, Application US/10673119
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael E.
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzieva, Olga
APPLICANT: Jeruzalmi, David
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US-10-673-119-25
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                                      32; Conservative
                                                                                                                                                                                                                                                                                                                                                                       L-ISELEEYIKN 115
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       Best Local Similarity
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US-10-673-120-25
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US-10-679-063-20147
Sequence 20147, Application US/10679063
Sequence 20147, Application US/10679063
Sequence 20147, Application US/10679063
SIGNATION: APPLICANTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15 (52054) B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 20147
LENGTH: 1378
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GENERAL INFORMATION:
APPLICANT: Edgerron, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)8
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
NUMBER OF SOO ID NOS: 27373
SEQ ID NO 18206
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                                                                                                                                                                                                                                                                                                                                    16.3%; Score 93.5; DB 6; Length 147; ilarity 28.4%; Pred. No. 9.3; Conservative 25; Mismatches 35; Indels
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   PRIOR APPLICATION NUMBER: US 60/329,140
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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                                                                                                                                                                     LENGTH: 147
TYPE: PRT
ORGANISM: Staphylococcus aureus
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US-10-679-063-20147
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Best Local Similarity
Matches 25; Conserv
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Matches 28; Conserv
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US-10-679-063-18206
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46

Gaps

41;

Length 260;

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14.2%; Score 81.5; DB 6; 22.8%; Pred. No. 70; cive 27; Mismatches 37;
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US-10-673-098-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: O'Donnell, Michael E. APPLICANT: Yuzhakov, Alexander
                                                                                                                                                                                                                                                                                                                                                                                               DTQKANIQKLISELEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                        207 DLSQGSLRDGLSLLDQ 222
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DLSQGSLRDGLSLLDQ 222
                                  Similarity 22.83
31; Conservative
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TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael E.
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Geruzalmi, David
APPLICANT: Bruck, Irina
APPLICANT: Bruck, Irina
APPLICANT: Kuriyan, John
TITLE OF INVENTION: ENTYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: 22221/1030
      APPLICANT: CLUCANT: N: CLUC
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Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37; Indels 4
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CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: US/09/716,964A
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/143,202
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR APPLICATION NUMBER: 09/057,416
PRIOR APPLICATION NUMBER: 09/057,416
PRIOR FILING DATE: 1998-04-08
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 260
TYPE: PRT
ORGANISM: Mycoplasma genitalium
US-10-671-134-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mycoplasma genitalium
US-10-673-120-25
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APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Urieva, Olga
APPLICANT: Bruck, Irina
APPLICANT: Bruck, Irina
APPLICANT: Bruck, Irina
APPLICANT: Kuriyan, John
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: USE THEREOF
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TITLE OF INVENTION: USE THEREOF
THE OF INVENTION UNMERR: US/09/716,964A
PRIOR FILING DATE: 1997-04-08
PRIOR APPLICATION NUMBER: 09/057,416
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
NUMBER OF SEQ ID NOS: 212
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                                                                                                                                                                                                                                                                --NEISSKEIAKCSE--FKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVT 95
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Length 260
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                                                                Indels
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Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37;
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APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
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TYPE: PRT
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APPLICANT: Bruck, Irina
APPLICANT: Bruck, Irina
APPLICANT: Kuriyan, John
TITLE OF INVENTION: BRIZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: BRIZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: UNBER: US/09/716,964A
PRIOR FILING DATE: 1097-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR APPLICATION NUMBER: 08/823,407
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PATCHILING UNIVER: US/05/7,416
NUMBER OF SEQ ID NOS: 212
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APPLICANT: Variation US/10670844
GENERAL INFORMATION:
APPLICANT: Variation-Strander
APPLICANT: Yuriation-Strander
APPLICANT: Yuriation-Strander
APPLICANT: Generalini, David
APPLICANT: Bruck, Irina
APPLICANT: Kuriyan, John
TITLE OF INVENTION: ENZYERS DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: USE THEREOF
FILLS REPRESENCE: 2221/1030
FILLS REPRESENCE: 2221/1030
CURRENT APPLICATION NUMBER: US/10/670,844
CURRENT FILING DATE: 2003-09-25
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14.2%; Score 81.5; DB 6; Length 2.
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37; Indels
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PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/143,202
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
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US-10-673-127-25
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 260
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US-10-670-844-25
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TRNGTH: 260
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APPLICANT: YULIGAYA, Olga
APPLICANT: YULIGAYA, Olga
APPLICANT: YULIGAYA, Olga
APPLICANT: BRUCK, Titha
APPLICANT: BRUCK, Titha
APPLICANT: BRUCK, Titha
APPLICANT: KULIYAN, JOHN
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: 22221/1030
CURRENT APPLICATION NUMBER: US/09/716,964A
PRIOR APPLICATION NUMBER: US/09/716,964A
PRIOR PILING DATE: 2000-11-21
PRIOR PILING DATE: 1997-04-08
PRIOR FILING DATE: 1998-04-08
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                                                                                                                                                                                                                                     47 ------NEISSKEIAKCSE--FKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVT
                                                           Gaps
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   Length 260;
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22.8%; Pred. No. 70;
tive 27; Mismatches 37; Indels
                                                        37; Indels
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                                                                                                                       4 INDINDLVNATFOVKKFFRDTKKKFNLNYBEIYILN--HILRSES
   DB 6;
14.2%; Score 81.5; DE 22.8%; Pred. No. 70; iive 27; Mismatches
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US-10-671-859-25
Sequence 25, Application US/10671859
GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael E.
APPLICANT: Yuzhakov, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/10671403 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Mycoplasma genitalium
US-10-671-403-25
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Best Local Similarity 22.8%
Matches 31; Conservative
   Query Match
Best Local Similarity 22.8
Matches 31; Conservative
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DTQKANIQKLISELEE 111
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207 DLSQGSLRDGLSLLDQ 222
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ORGANISM: Borrelia burgdorferi
US-10-688-058-60
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244 KIKSVEYKKILEELD 258
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APPLICANT: Yurieva, Olga
APPLICANT: Jeruzalmi, David
APPLICANT: Jeruzalmi, David
APPLICANT: Jeruzalmi, David
APPLICANT: Buck, Intina
APPLICANT: Kuriyan, John
TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: 22221/1030
CURRENT APPLICATION NUMBER: US/10/671,859
CURRENT FILING DATE: 2000-11.21
PRIOR APPLICATION NUMBER: US/09/716,964A
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
NUMBER OF SEQ ID NOS: 212
SOCTWARE: SEQ ID NOS: 212
SEQ ID NO 25
LENGTH: 260
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GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael E.
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Wirthan, John
ITILE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
ITILE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
ITILE OF INVENTION: USE THEREOF
ITILE OF INVENTION: USE THEREOF
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ITILE OF INVENTION UNMERS: US/10/671,412
CURRENT FILING DATE: 2000-11-21
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1998-04-08
PRIOR FILING DATE: 1998-04-08
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 25:
LENGTH: 260
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14.2%; Score 81.5; DB 6;
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37;
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US-10-671-859-25
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Sequence 60, Application US/10688058

Sequence 60, Application US/10688058

GENERAL INFORMATION:
APPLICANT: SYKES, KATHRYN F.
APPLICANT: HALE, KATHRYNE S.
APPLICANT: JOHNSTON, STEPHEN A.
TITLE OF INVENTION: MCTHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
TITLE OF INVENTION: BORREIA
FILE OF INVENTION: BORREIA
FILE OF INVENTION: BORREIA
FILE REPERENCE: MCRO:003US
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 141
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 60.
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Sequence 259, Application PC/TUS0327401
GENERAL INFORMATION:
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS, TREATMENT AND TITLE OF INVENTION: PREVENTION OF ACTIVE INFECTION
FILE REFERENCE: 70035-5241-PCT
CURRENT PILIAGIANION NUMBER: PCT/US03/27401
PRIOR PAPLICATION NUMBER: US 60/407,082
PRIOR PLICATION NUMBER: US 60/407,082
PRIOR FILLING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 560
SOFTWARE: Patentin version 3.2
LENGTH: 428
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Length 260;
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13.9%; Score 80; DB 6; Length 112
Best Local Similarity 22.2%; Pred. No. 2.1e+02;
Matches 30; Conservative 27; Mismatches 50; Indels
                                                              Indels
                                                                                                                 4 INDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILN--HILRSES
                                                        27; Mismatches 37;
   DB 6;
Query Match
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches
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; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
PCT-US03-27401-259
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Length 42	Indels
3 1;	36;
13.9%; Score 79.5; DB 1; Length 428; 25.8%; Pred. No. 1.3e+02;	20; Mismatches
13.9%;	ative 2
Query Match 13.9%; Best Local Similarity 25.8%;	ches 24; Conserva
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Search completed: November 17, 2003, 12:49:36 Job time : 68 secs

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